

FIG. I

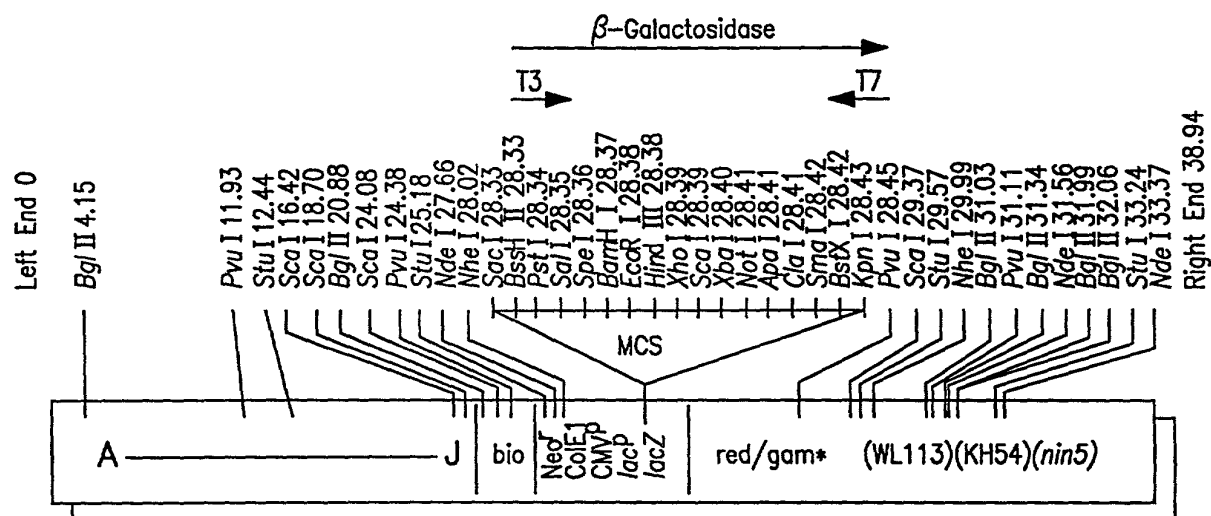


FIG. 2A

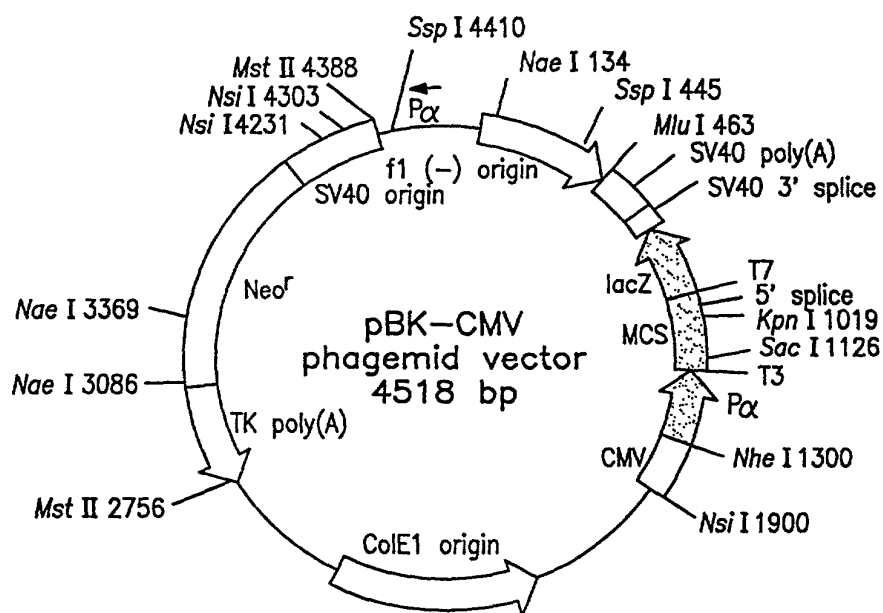


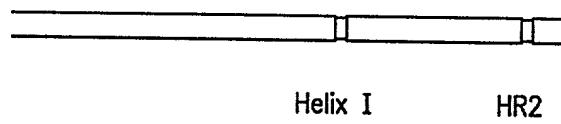
FIG. 2B

QC-RT-PCR primers for the 5' coding sequence of
Candida tropicalis 20336 P450CYP52A5A

5'	ATGATTGAACAACCTCCTAGAAATATTGGTAT	GTCGTTGTGCCAGTGTGTACATCATCAAA	CAACTCCTTGCATACACAAGACTCGCGTC	3'	90
3'	TACTAAGCTTTGAGGATCTTATAACCAT	CAGCAACACGGTCACAACATGTAGTAGTT	GTTGAGGAACGTATGTGTTTCTGAGCGCAG	5'	
5'	TTGATGAAAAAGTTGGGTGCTGCTCCAGTC	ACAAACAAGTTGTACGACAACGGTTTCGGT	ATCGTCAATGGATGGAAGGCTCTCCAGTTC	3'	180
3'	AACTACTTTTCAACCCACGACGAGGTGAG	TGTTTGTTCACAACATGCTGTGCGAAAGCCA	TAGCAGTTACCTACCTTCCGAGAGGTCAAG	5'	
Forward Primer 7581-97F					
5'	AAGAAGAGAGGGCAGGGCTCAAGAGTACAAC	GATTACAAAGTTTGACCACTCCAAGAACC	AGCGTGGGCACCTACGTACGTATCTTTTC	3'	270
3'	TTCTTTCTCCCGTCCCGAGTTCTCATGTG	CTAATGTTCAAACCTGGTGAGGTTCTTGGGT	TCGCACCCGTGGATGCAGTCATAAGAAAAAG	5'	
5'	GGCACGAGATCGTCGTGACCAAGATCCA	GAGAAATATCAAAGCTATTTTGGCAACCCAG	TTTGGTGATTTTCTTTTGGCAAGAGGCAC	3'	360
3'	CCGTGGTCCTAGCAGCACCTGGTTCTAGGT	CTCTTATAGTTTCGATATAAACCGTTGGGTC	AAACCACTAAAAAAGAAACCCGTTCTCCGTG	5'	
5'	ACTCTTTTAAAGCCTTTGTTAGGTGATGGG	ATCTTCACATTGGACGGCGAAGGCTGGAAG	CACAGCAGAGCCCATGTTGAGACCAAGTTT	3'	450
3'	TGAGAAAAAATTCGGAAACAATCACTACCC	TAGAAAGTGAACCTTCCCGCTTCCGACCTTC	GTGTCGTCTCGGTACAACCTCTGGTGTCAAA	5'	
Reverse Primer 7581-97M					
5'	GCCAGAGAACAAAGTTGCTCATGTGACGTG	TTGGAACCAACACTTCCAGTTGTTGAAGAAG	CATATTCTTAAGCACAAGGGTGAATACTTT	3'	540
3'	CGGTCTCTTGTTCACGAGTACACTGCAGC	AACCTTGGTGTGAAGGTCAACAACCTTCTTC	GTATAAGAATTCGTGTTCCCACTTATGAAA	5'	

FIG. 3

CYP Gene



CPR Gene

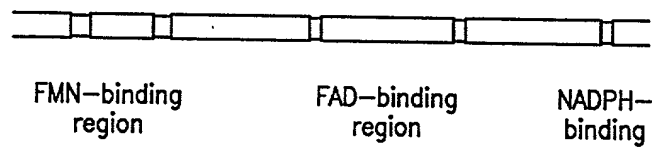


FIG. 4

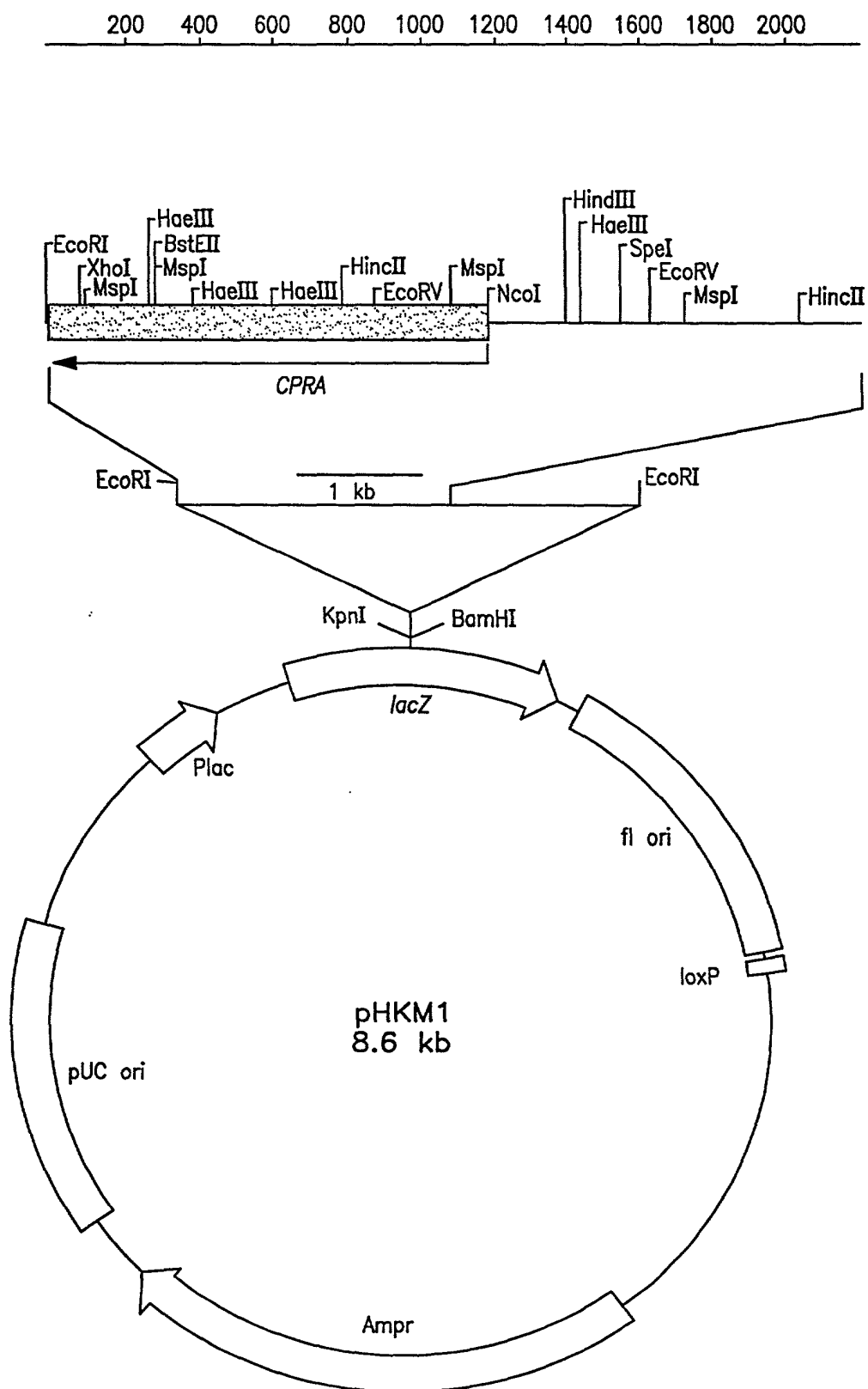


FIG. 5

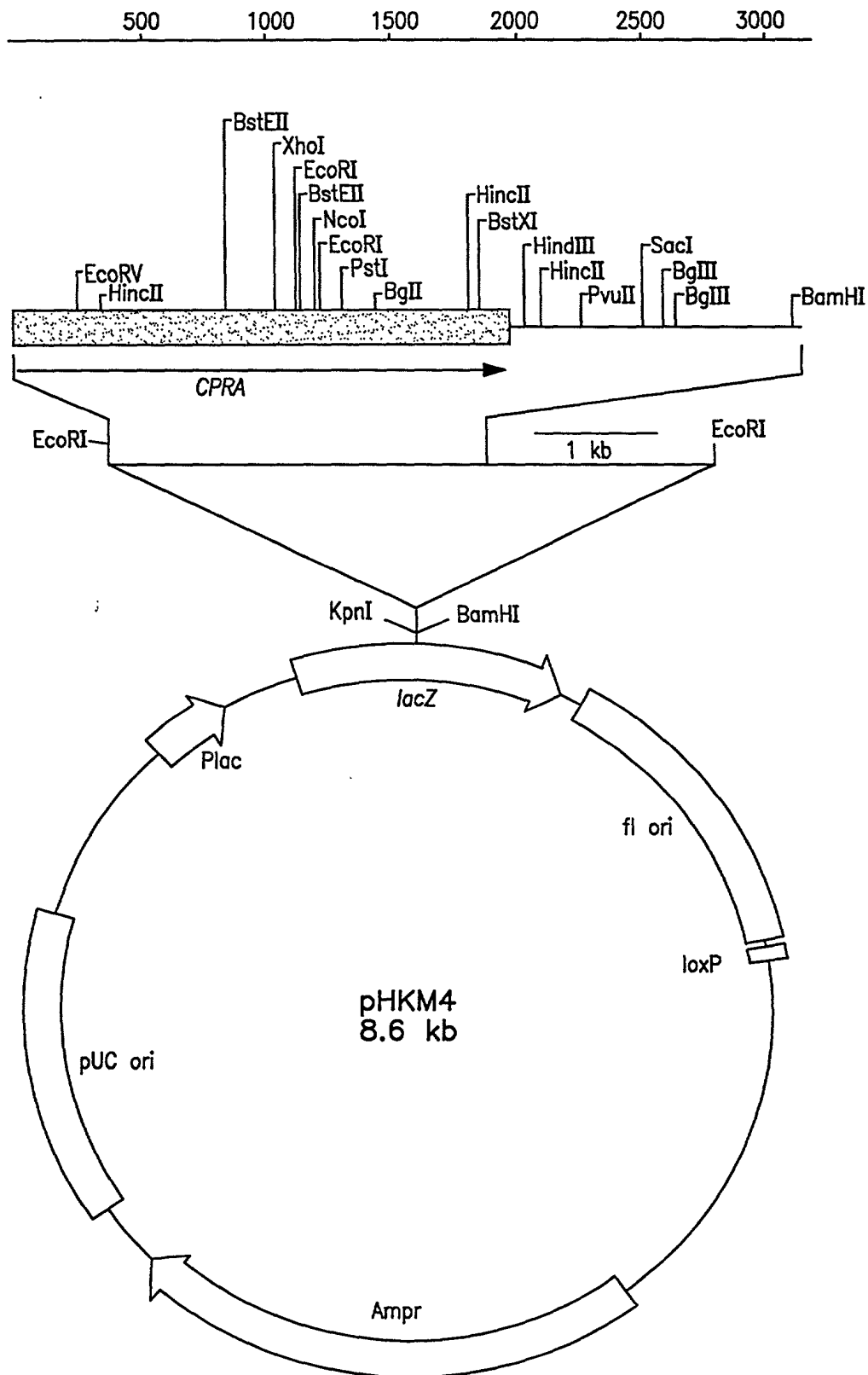


FIG. 6

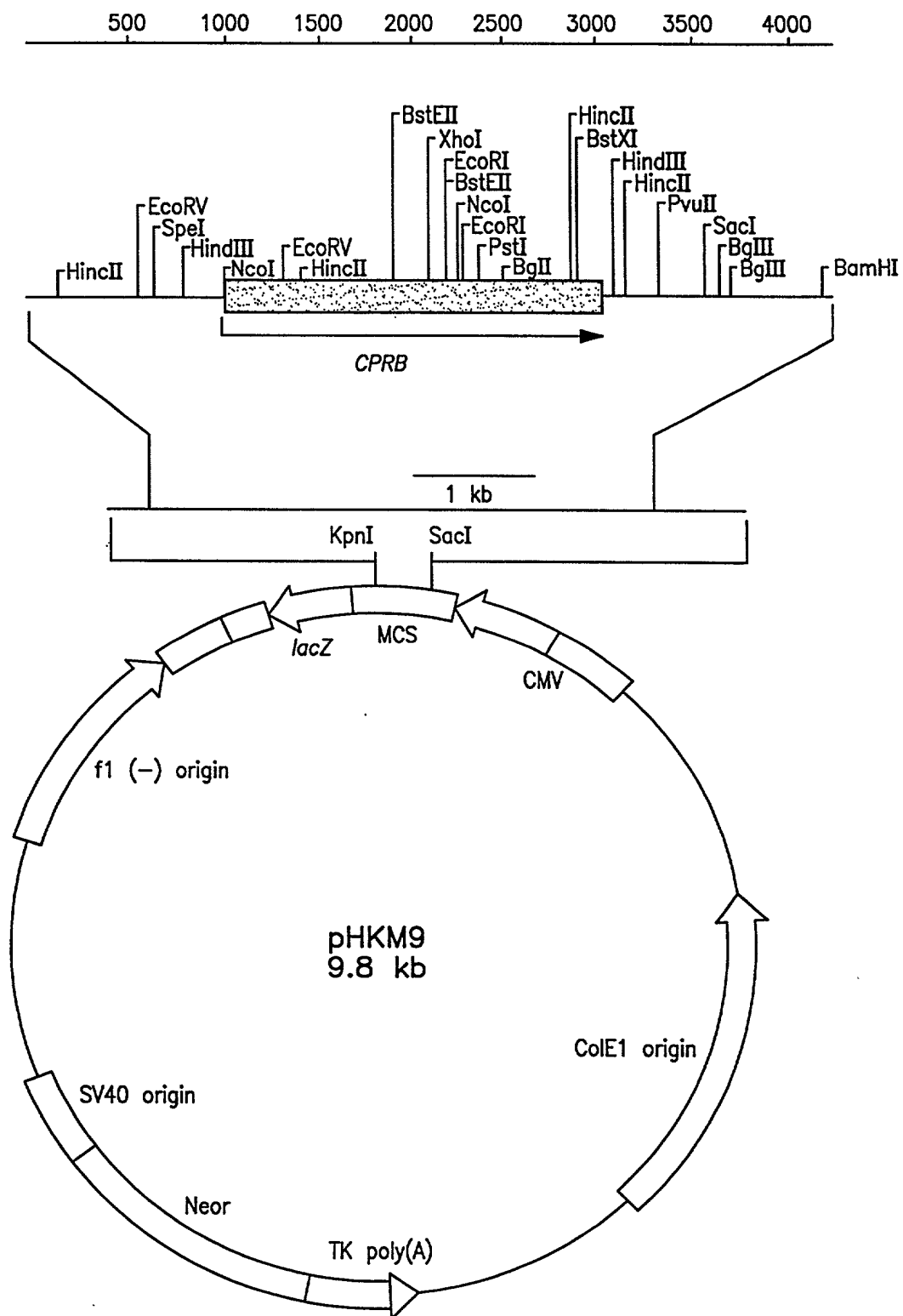


FIG. 7

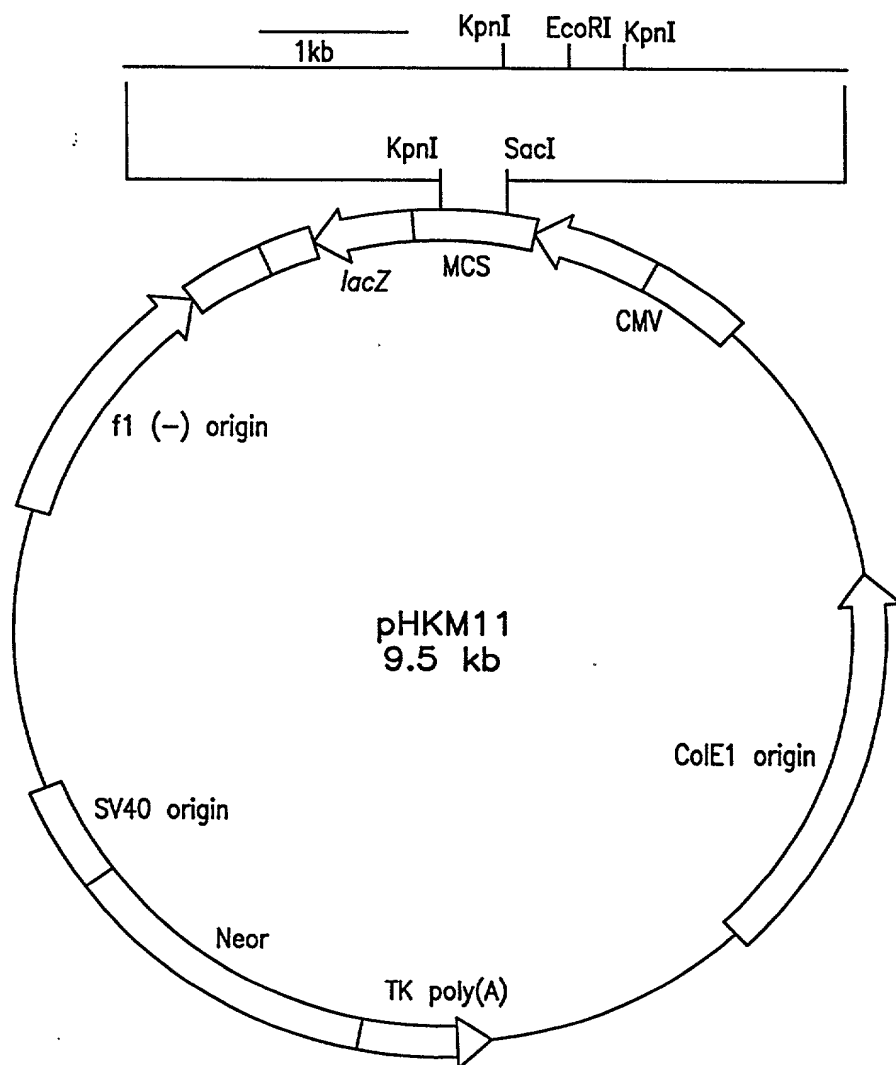
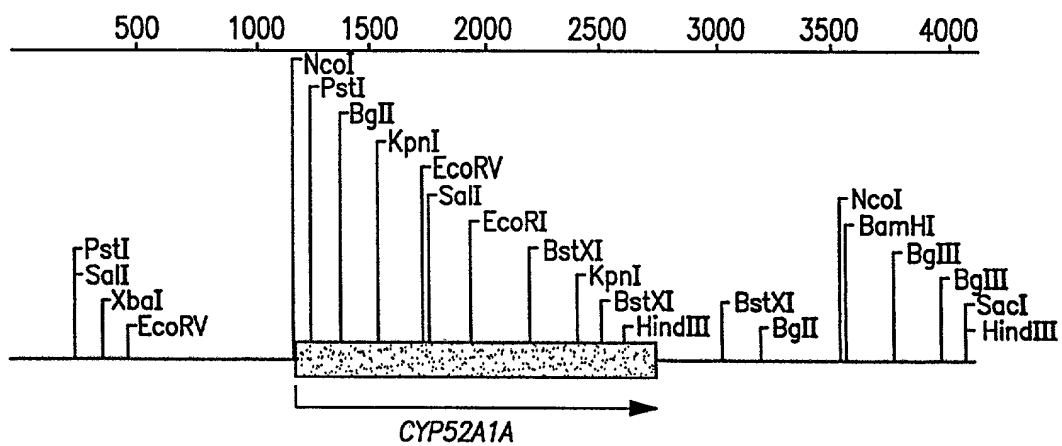


FIG. 8

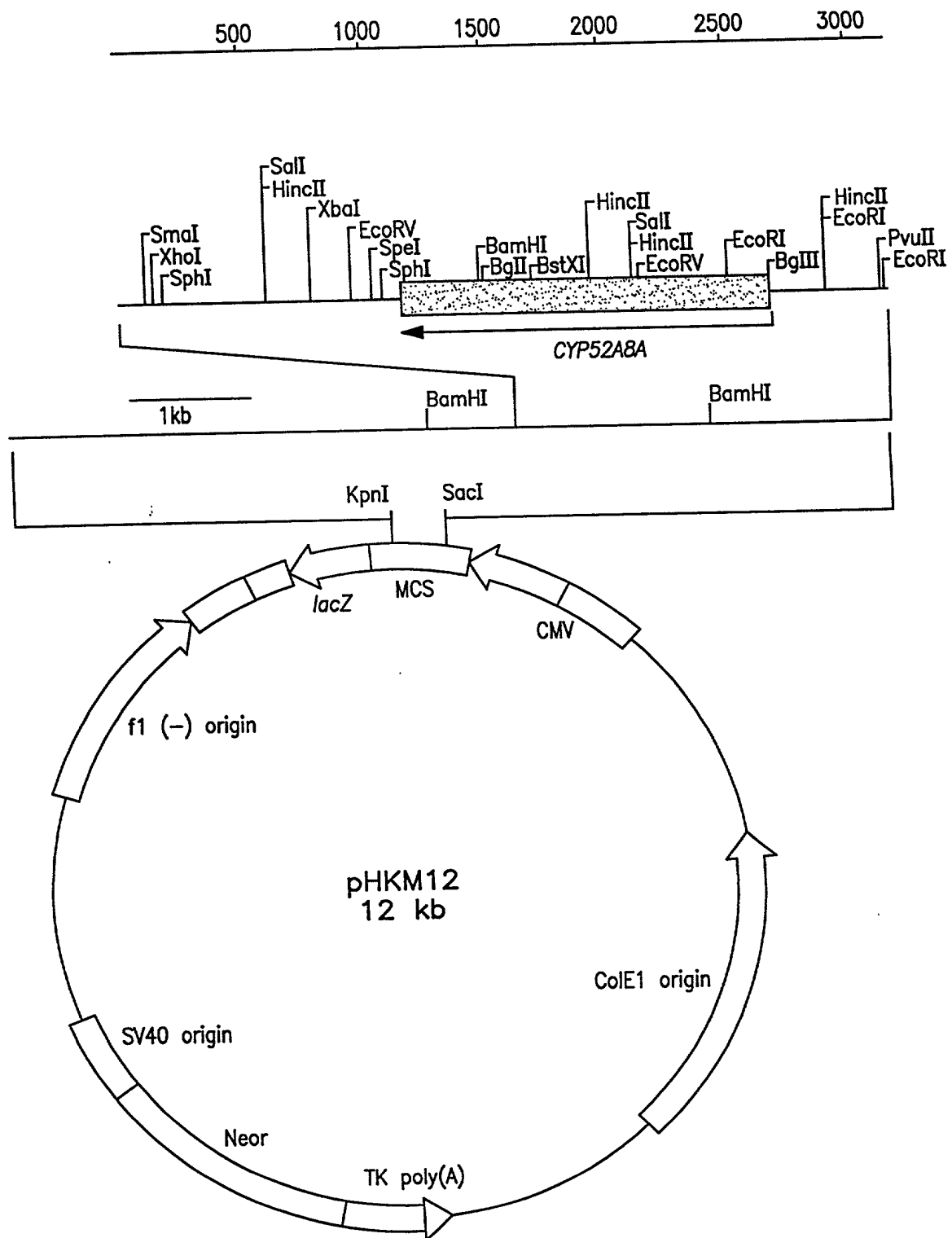


FIG. 9

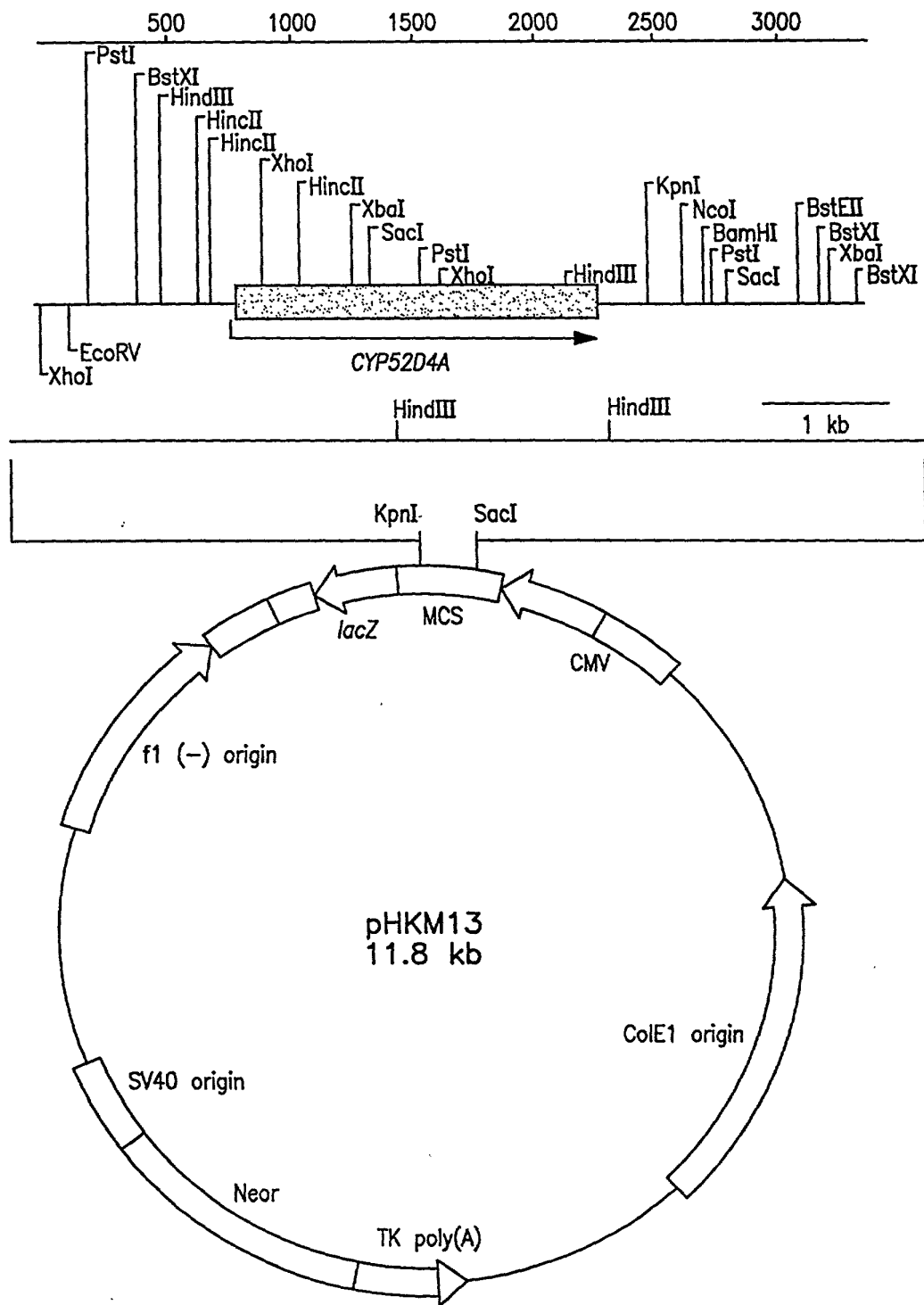


FIG. 10

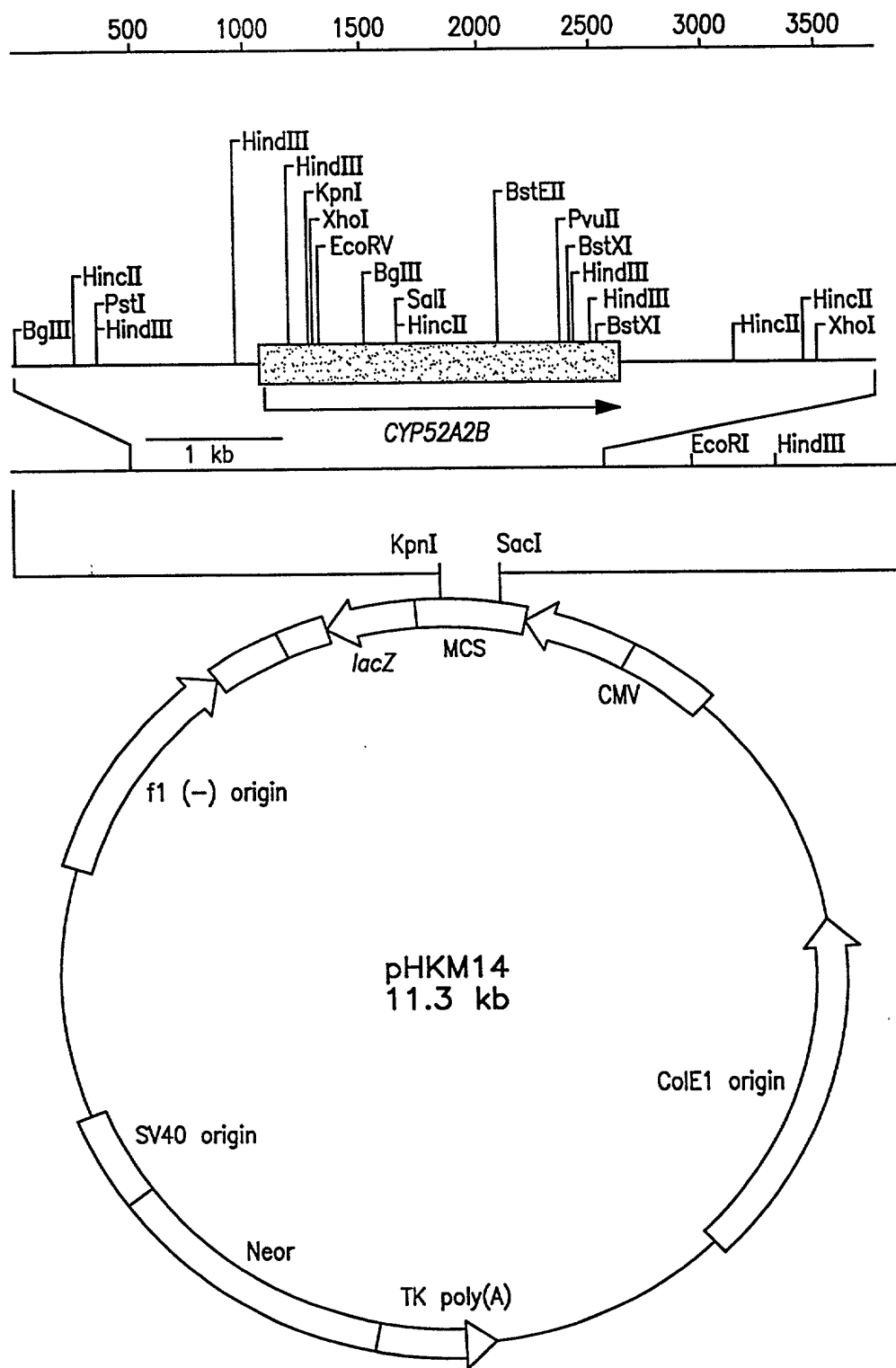


FIG. 11

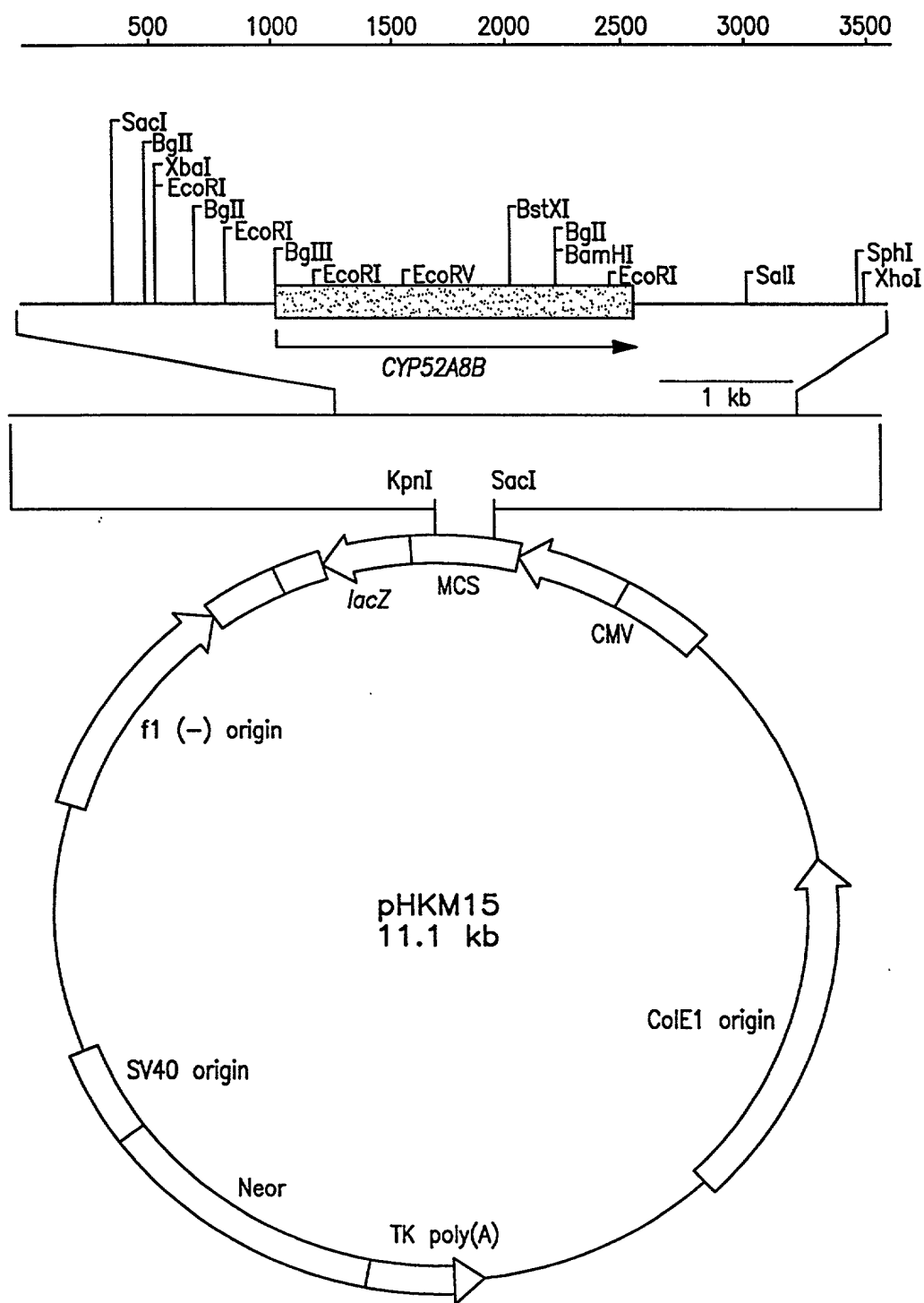


FIG. 12

C. tropicalis 20336 CPR Allele DNA Alignment of DS Sequence

CPRB	1	TATATGATATATGATATATCTTCCTGTGTAATTATTATTTCGTATTTCGTTAATACTTACTACATTTT	5	CATCA
CPRB	1		70	*
CPRB	6	AGATCATCTATGGGGATAATTA-----CGACAGCAACATTGCAGAAAAGCGTTGGTCACAATCGAAAGA	70	
CPRB	71	TCTTTATTTATGAAGAAAAGGAGAGTTTCGTAAGTTGAGTTGAGTAGAATAAGGCTGTTGTGCATACGGGGA	140	
CPRB		* ** *** ** ** *		**
CPRB		* ** *** ** ** *		**
CPRB		* ** *** ** ** *		**
CPRB	71	GCCTAIG-GCGTTGCCGTCGTTGAGGCAAAATGACAGCAC--CAACAATAACGATGTCCTCCAGTGAAGAGC	137	
CPRB	141	GCAGAGGAGAGTATCCGACGAGAGGAACTGGGTGAAATTTTCATCTATGCTGTTGCCGTCCTGTACTGTAC	210	
CPRB		** * * * * *		*
CPRB		** * * * * *		*
CPRB		** * * * * *		*
CPRB	138	CTTCAGAACAGTCCATTGTTGACGCT--TAAGGCACGGATAATTACGTGGGGCAAGAAAGGCGGAATTA	205	
CPRB	211	TGTAAATCTTAGATTTCCTAGAGGTTGTTCTAGCAAAATAAAGTGTTCAGATACAAATTTTACAGGCAAG	280	
CPRB		* *		*
CPRB		* *		*
CPRB		* *		*
CPRB	206	GTTATGGGGGGATCAAA--AGCGGAAGATTGTTGTTGCTTGTGGGTTTTTTCCTTTATTTTTCATATGAT	273	
CPRB	281	GGTAAAGGATCAACTGATTAGCGGAAGATTGGTGTTCCTGTTGGGTTCTT--TTATTTTTCATATGAT	347	
CPRB		* ** ** *		*
CPRB		* ** ** *		*
CPRB		* ** ** *		*
CPRB	274	TTCTTTGCGCAAGTAAACATGTGCCAATTAGTTTGTGATTAGCGTGCC-CCACAATTGGCATCGTGGACG	342	
CPRB	348	TTCTTTGCGCGAGTAAACATGTGCCAATCTAGTTTATGATTAGCGGTACCTCCACAATTGGCATCTTGGACG	417	
CPRB		*****		*
CPRB		*****		*
CPRB		*****		*
CPRB	343	GGCGTGTGTTGTATACCCCAAGTCTTAACCTAGCTCCAGTCTCGACGGTGTCTCGACGATGTCCTTCTT	412	
CPRB	418	GGCGTGTGTTGTCTTACCCCAAGCCTTATTTAGTTCACAGTCTCGACGGTGTCTCGCCGATGTCCTTCTC	487	
CPRB		*****		*
CPRB		*****		*
CPRB		*****		*

FIG. 13A-I

[illegible]

FIG. 13A-3

CPRA	1523	AAGGTGGTGACAGGTTTGTGTAATACGCTGAAGTGATGACGGTACTGGCACCTTGGACGAAGATTTCAT	1592
	1550	AAGGTGGTGACAGATTGTCTGAATATGCTGAAGGTGACGCGGCACTTGGCACCTTGGACGAAGATTTCAT	1619

CPRA	1593	GGCCTGGAAGGACAATGTCTTTTGA CGCCTTGAAGAAATGAATTGAACCTTTGAAGAAAAGGAATTGAAGTAC	1662
	1620	GGCCTGGAAGGATAATGTCTTTGACGCGCTTGAAGAAATGACTTTGAACCTTTGAAGAAAAGGAATTGAAGTAC	1689

CPRA	1663	GAACCAAAACGTGAAATTGACTGAGAGAGACGACTTGTCTGTGCTGACTCCCAAGTTTCCTTGGGTGAGC	1732
	1690	GAACCAAAACGTGAAATTGACTGAGAGAGATGACTTGTCTGTGCTGCCGACTCCCAAGTTTCCTTGGGTGAGC	1759

CPRA	1733	CAACAAGAAAGTACATCAACTCCGAGGGGATCGACTTGACCAAGGGTCCATTGACCCACACCCACCCATA	1802
	1760	CAACAAGAAAGTACATCAACTCCGAGGGGATCGACTTGACCAAGGGTCCATTGACCCACACCCACCCATA	1829

CPRA	1803	CTTGGCCAGAAATCACCGAGACGAGAGATTGTTTCAGCTCCAAGGACAGACACTGTATCCACGTTGAATTT	1872
	1830	CTTGGCCAGGATCACCGAGACGAGAGATTGTTTCAGCTCCAAGGAAAGACACTGTATTCACGTTGAATTT	1899

CPRA	1873	GACATTTCTGAATCGAACTTGAAATACACCAACCGGTGACCATCTAGCTATCTGGCCATCCAACTCCGACG	1942
	1900	GACATTTCTGAATCGAACTTGAAATACACCAACCGGTGACCATCTAGCCATCTGGCCATCCAACTCCGACG	1969

CPRA	1943	AAACATTAAGCAATTGCGCAAGTGTTCGGATTGGAAGATAAACTCGACACTGTTATTGAATTGAAGGC	2012
	1970	AAACATCAAGCAATTGCGCAAGTGTTCGGATTGGAAGATAAACTCGACACTGTTATTGAATTGAAGGC	2038

FIG. 13B-2

CPRA	2223	CATTGCCGATGCCTTGTATATTCCTCCAACAACGCTCCATGGTCCGATGTTCCCTTTTGAATTCCTTATT	2292
	2250	CATTGCCGATGCCTTGTATATTCCTCCAACAACACTCCATGGTCCGATGTTCCCTTTTGAATTCCTTATT	2319
CPRA	2293	GAAAACGTTCCACACTTGACTCCACGTTACTACTCATTTCGTCTTCGTCACTGAGTGAAAAGCAACTCA	2362
	2320	GAAAACATCCAACACTTGACTCCACGTTACTACTCATTTCGTCTTCGTCACTGAGTGAAAAGCAACTCA	2389
CPRA	2363	TCAACGTTACTGCAGTTGTTGAAGCCGAAGAAGCTGAAGGCAGACCAAGTCACTGGTGTGTGCACCAA	2432
	2390	TCAATGTTACTGCAGTCGTTGAGGCCGAAGAAGCCGATGGCAGACCAAGTCACTGGTGTGTGCACCAA	2459
CPRA	2433	CTTGTGAAGAACGTTGAAATTGTGCAAAACAAGACTGGCGAAAAGCCACTTGTCCACTACGATTGAGC	2502
	2460	CTTGTGAAGAACATTGAAATTGCGCAAAACAAGACTGGCGAAAAGCCACTTGTTCACACTACGATTGAGC	2529
CPRA	2503	GGCCCAAGAGGCAAGTTCAACAAGTTCAAGTTGCCAGTGATGTGAGAAGATCCAACTTTAAGTTGCCAA	2572
	2530	GGCCCAAGAGGCAAGTTCAACAAGTTCAAGTTGCCAGTGACACGTGAGAAGATCCAACTTTAAGTTGCCAA	2599
CPRA	2573	AGAACTCCACCACCCAGTTATCTTGATTGGTCCAGGTACTGGTGTGCCCCCATTTGAGAGGTTTGTTCAG	2642
	2600	AGAACTCCACCACCCAGTTATCTTGATTGGTCCAGGTACTGGTGTGCCCCCATTTGAGAGGTTTGTTCAG	2669
CPRA	2643	AGAAAGAGTTCAACAAGTCAAGAATGGTGCAATGTTGGCAAGACTTTGTGTTTATGTTGTCAGAAAC	2712
	2670	AGAAAGAGTTCAACAAGTCAAGAATGGTGCAATGTTGGCAAGACTTTGTGTTTATGTTGTCAGAAAC	2739

FIG. 13C-1

CPRA	2713	TCCAAACGAGGACTTTTGTACAAGCAAGAATGGCCGAGTACGCTTCTGTTTGGGTGAAAACTTTGAGA	2782
CPRB	2740	TCCAAACGAGGACTTTTGTACAAGCAAGAATGGCCGAGTACGCTTCTGTTTGGGTGAAAACTTTGAGA	2809

CPRA	2783	TGTTCAATGCCCTTCTCCAGACAAGACCCCATCCAAGAAAGTTTACGTCCAGGATAAGATTTTAGAAAAACAG	2852
CPRB	2810	TGTTCAATGCCCTTCTCTAGACAAGACCCCATCCAAGAAAGTTTACGTCCAGGATAAGATTTTAGAAAAACAG	2879

CPRA	2853	CCAACTTGTGCACGAGTTGTTGACTGAAGGTGCCATTATCTACGTCTGTGGTGATGCCAGTAGAATGGCT	2922
CPRB	2880	CCAACTTGTGCACGAAATTGTTGACCGAAGGTGCCATTATCTACGTCTGTGGTGACGCCAGTAGAATGGCC	2949

CPRA	2923	AGAGACGTGCAGACCACAAATTTCCAAGATTGTTGCTAAAAGCAGAGAAATTAGTGAAGACAAGGCTGCTG	2992
CPRB	2950	AGAGACGTGCAGACCACGATCTCCAAGATTGTTGCCAAAAGCAGAGAAATCAGTGAAGACAAGGCCGCTG	3019

CPRA	2993	AATTGGTCAAGTCCCTGGAAGGTCCAAAATAGATACCAAGAAGATGTTTGGTAGACTCAAACGAAATCTCTC	3062
CPRB	3020	AATTGGTCAAGTCCCTGGAAGGTCCAAAATAGATACCAAGAAGATGTTTGGTAGACTCAAACGAAATCTCTC	3089

CPRA	3063	TTTCTCCCAACGCATTATGAATCTTTATTTCTCATTTGAAGCTTTACATATGTTCTACACTTTATTTTTT	3132
CPRB	3090	TTTCTCCCAACGCATTATGA - - - TATTCTCATTTGAAGTTTACATATGTTCTATAATTTCAATTTTTT	3155

CPRA	3133	TTTTTTTTTTTATTATTATATTACGAAACATAGGTCAACTATATATACTTGATTAAATGTTATAGAAACAA	3202
CPRB	3156	TTT - - - - - ATTATATTACGAAACATAGGTCAACTATATATACTTGATTAAATGTTATAGAAACAA	3215

FIG. 13C-2

CPRA	3203	TAACTATTATCTACTCGTCTACTTCTTTGGCATTTGACATCAACATTACCGTTCCCATTTACCGTTGCCGTT	3272
CPRB	3216	TAAATTATTACTACTCGTCTACTTCTTTGGCATTTGGCATTTGGCATTTGGCATTTGCCGTTGCCGTT	3285
		*** ****	**** *
CPRA	3273	GGCAATGCCGGGATATTTAGTACAGTATCTCCAAATCCGGATTTGAGCTATTGTAGATCAGCTGCAAGTCA	3342
CPRB	3286	GGTAATGCCGGGATATTTAGTACAGTATCTCCAAATCCGGATTTGAGCTATTGTAAATCAGCTGCAAGTCA	3355
		** ****	*****
CPRA	3343	TTCTCCACCTTCAACCCAGTACTTATACTTTCATCTTTGACTTCAAGTCCAAAGTCATAAATATTACAAGTTA	3214
CPRB	3356	TTCTCCACCTTCAACCCAGTACTTATACTTTCATCTTTGACTTCAAGTCCAAAGTCATAAATATTACAAGTTA	3425
		*****	*****

FIG. 13C-3

CPRA	3903	CTCCTGGTTCCCTCATAGTACAACTGGCACTTCTTCGAGAGGCTCAATTCCTCGTAGTTCCCGTCCAAG	3972
CPRB	3916	CTCCTGGTTCCCTTTCATAGTACAACTGGCACTTCTTCGAGAGACTCAACTCCTCGTAGTTCCCGTCCAAG	3985
		*****	*****
CPRA	3973	ATATTCGGCAACAAGAGCCCCGTACCGCTCACGGAGCATCAAGTCGTGGCCCTGGTTGTTCAACTTGTGA	4042
CPRB	3986	ATATTCGGCAACAAGAGCCCCGTAGCGCTCACGGAGCATCAAGTCGTGGCCCTGGTTGTTCAACTTGTGA	4055
		*****	*****
CPRA	4043	TGAAGTCCGAGGTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGGAACAAGTCTTGCATTTTAG	4112
CPRB	4056	TGAAGTCCGATGTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGGAACAAGTCTTGCATTTTAG	4125
		*****	*****
CPRA	4113	CTCGATGAAGTCGTACAACTCACACGTCGAGATATACTCCTGTTCTCCTTCAAGAGCCGGATCCGCAAG	4182
CPRB	4126	CTCGATGAAGTCGTACAACT	4125
		*****	*****
CPRA	4183	AGCTTGTGCTTCAAGTAGTCGTTG	4206
CPRB	4146		4145

FIG. 13D-2

CPRB	MALDKLDLYVITLVVAAAYFAKNQFLDQPDQTGFLNTDGSNSRDVLLTLKNNKNTL	60
CPRB	MALDKLDLYVITLVVAAAYFAKNQFLDQPDQTGFLNTDGSNSRDVLLTLKNNKNTL	60
CPRB	LLFGSQTGTAEDYANKLSRELHSRFGKLTWADFADYDWDNFGDITEDILVFFIVATYGE	120
CPRB	LLFGSQTGTAEDYANKLSRELHSRFGKLTWADFADYDWDNFGDITEDILVFFIVATYGE	120
*		
CPRB	GEPTDNADEFHTWLTTEEADTLSTLKYTVFGLGNSTYEFFNAIGRKFDRLLSEKGGDRFAE	180
CPRB	GEPTDNADEFHTWLTTEEADTLSTLRYTVFGLGNSTYEFFNAIGRKFDRLLSEKGGDRFAE	180
CPRB	YAEAGDDGTGLDEDFMAWKDNVFDALKNDLNFEEKELKYEPNVKLTERDDLAAADSQVSL	240
CPRB	YAEAGDDGTGLDEDFMAWKDNVFDALKNDLNFEEKELKYEPNVKLTERDDLAAADSQVSL	240
*		
CPRB	GEPNKKYINSEGIDLTGPFDPHTHPYLARIETETRELFSKDRHCHIVEFDISESNLKYYT	300
CPRB	GEPNKKYINSEGIDLTGPFDPHTHPYLARIETETRELFSKDRHCHIVEFDISESNLKYYT	300
CPRB	GDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTITYGAVIRHLE	360
CPRB	GDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTITYGAVIRHLE	360
*		
CPRB	ISGPVSRQFFLSIAGFAPDEETKKAFTRLGGDKQEFKATVTRRKFNIAADALLYSSNNAPW	420
CPRB	ISGPVSRQFFLSIAGFAPDEETKKTFTRLGGDKQEFKATVTRRKFNIAADALLYSSNNTPW	420
**		
CPRB	SDVPFEFLIENVPHLTPRYYSISSSSLSSEKQLINVTAVVEAEAEADGRPVTGVVTNLLKN	480
CPRB	SDVPFEFLIENIQHLTPRYYSISSSSLSSEKQLINVTAVVEAEAEADGRPVTGVVTNLLKN	480

FIG. 14A

	*	*	
CPR A	VEIVQNKTGEKPLVHYDLSGPRGKFNKFKLPVHVRRSNFKLPKNSTTPVILIGPGTGVAP	540	
CPR B	IEIAQNKTGEKPLVHYDLSGPRGKFNKFKLPVHVRRSNFKLPKNSTTPVILIGPGTGVAP	540	
CPR A	LRGFVRERVQQVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNAFSRQ	600	
CPR B	LRGFVRERVQQVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNAFSRQ	600	
CPR A	DPSKKVYVQDKILENSQLVHELLTEGAI IYVCGDASRMARDVQTTISKIVAKSREISEDK	660	
CPR B	DPSKKVYVQDKILENSQLVHELLTEGAI IYVCGDASRMARDVQTTISKIVAKSREISEDK	660	
CPR A	AAELVKSWKVQNRVYQEDVW	680	
CPR B	AAELVKSWKVQNRVYQEDVW	680	

FIG. 14B

[illegible]

FIG. 15A-1

CYP52A1A	60	GAAACACAAATGACAACTCCTGCGTAACTTGC	129
CYP52A2A	141	CTTGTTCGGTCAACCATTCCTTGGTGTGGTGC	210
CYP52A2B	1	GCTCAACAAATTGCTGACAAAGATCTC	26
CYP52A3A	82	AAACTCTAGTATAATGGTGATAACTGGTTGCA	151
CYP52A3B	1	GCCAGACTTGCTCACTTTTGACTCCCTTCGAA	0
CYP52A5A	8	GCCAGACTTGCTCACTTTTGACTCTCTTAGAA	77
CYP52A5B	83	AAAAACCGATACAAGAAAGACAGTCAA	152
CYP52A8A	1		0
CYP52A8B	1		28
CYP52D4A	1		0
CYP52A1A	130	GACCTCCAGTCAAACGGACAGACAGACAAACA	199
CYP52A2A	211	GCAACACAAAGGCTAACGCCCTGGTTGTTGA	280
CYP52A2B	27	GCAACACAAAGGCTAACGCCCTGGTTGTTGA	96
CYP52A3A	152	ATATTTAATAAGCGTAGGAGTATAGGATGCAT	221
CYP52A3B	1	CGTATCTACCCGGGGTACCAACGAAACATGA	8
CYP52A5A	78	CGTATCTACCCGGGGTACCAACGAAACATGA	145
CYP52A5B	153	CGTATCTACCCGGGGTACCAACGAAACATGA	220
CYP52A8A	1	CAAGAACGTTAATGTCAACCAAGCGCCCAAG	0
CYP52A8B	29		96
CYP52D4A	1		0

FIG. 15A-2

CYP52A1A	200	TGTTAGACGACGGTTTCTTGCAAAGAC - AGGTGTTGGCATCTCGTACGATGGCAACTGCAGGAGGTGTCTG	268
CYP52A2A	281	AGATGCTCATTGAAGTACACCCAGAGCCATTTTGGACGCTATCCACTCTCTGGTGAAATTGTCCAAGGTTGAAT	350
CYP52A2B	97	AGATGTTCAATTGAAGTACACCCAGAGCCATTTTGGACGCTATCCACTCTGGTGAAATTGTCCAAGGTTGAAT	166
CYP52A3A	222	AAATTTTGTAATTCAGTAGGATTTTCATCAAAATTCGCAACCAATCTGGCGAAATAAATGATTCCTTTTAC	291
CYP52A3B	9	ATTCGCGGCCGTCGACAGAGTAGCAGTTATGCAAGCATGTGATTGTGGTTTTTGCAACCTGTTTGCAC	78
CYP52A5A	146	AGGCA - AAGACGGCAAGGAACCTATCT - TGGTGCAGAAAGGACAGTCCGTTGGGTTGATTACTATTGCCA	213
CYP52A5B	221	AGGCA - AAGACGGTAAGGAACCTATTT - TGGTGCAGAAAGGCCAGTCCGTTGGGTTGATTACTATTGCCA	288
CYP52A8A	1		0
CYP52A8B	97	CCATG - ATGTTTATGTTCTGGAGAGGT - TTTTCAAGGAATCGTCAATCCTCCGCCACCACCAAGAACCA	164
CYP52D4A	1		0

FIG. 15A-3

CYP52A1A	269	ACTTCTCCTTTAGGCAATAGAAAAAGACTAAGAGAAACAGCGTTTTTACAGGTTGCATTGGTTAATGTAGT	338
CYP52A2A	351	ACGAAACTTTCCCGAGTCTTCAACTTGAATGTCCCAACCTCCTGTCCAGGTGTCCCAAGTGAAATCTTGAA	420
CYP52A2B	167	ACGAGACTTTCCCGAGTCTTCAACTTGAATGTCCCAACCTCCTGTCCCGAGGTGTCCCAAGTGAAATCTTGAA	236
CYP52A3A	292	GTCAAAAGCTGA-ATAGTGCAGTTTAAAGCACCTAAATCACATATACAGCCTCTAGATACGACAGAGAA	360
CYP52A3B	79	GACAAATGATCG-ACAGT-CGATT--ACGTAATCCATATTATTAGAGGGGTAAATAAATAAATGGCA	144
CYP52A5A	214	CGCAGACGGACCCAGAGTATTTTGGGGCCGACGCTGGTGAGTTTAAGCCGGAGAGATGGTTTGATTCA--	281
CYP52A5B	289	CGCAGACGGACCCAGAGTATTTTGGGGCCGAGATGCTGGTGAGTTCAACCCGGAGAGATGGTTTGATTCA--	356
CYP52A8A	1	GTAAACGAGATCCATATTCAACAACCCACCGCAAGGTGACAAATGCTCAACAACAACAGCAACAACA--	0
CYP52A8B	165		232
CYP52D4A	1		0
CYP52A1A	339	ATTTTTTTAGTCCCAGCATTTCTGTGGGTTGCTCTGGGTTTCTAGAAATAGGAAATCACAGAGAAATGCAAA	408
CYP52A2A	421	CCCAACCAAGGCTGGACCGG-AAGGTGTTGACTCCTTCAACAAGGAAATCAAGTCTTTGGCTGGTAAGT	489
CYP52A2B	237	CCCAACCAAGGCTGGACCG--AAGGTGTTGACTCCTTCAACAAGGAAATCAAGTCTTTGGCTGGTAAGT	304
CYP52A3A	361	GCTCTTTATGATCTGAAGAAAGCATTAGAATAGCT--ACTATGAGCCACTATTTGGTGATATATATTAGGA	427
CYP52A3B	145	GCC---AGAAATTCAAAACATTTTGCAAAACAATGCAAAAGATGAGAAACTCCAACAGAAAAAATAAAAAA	210
CYP52A5A	282	AGCATGAAGAACTTGGGGTGTAATACTTGCCGTTCAATGCTGGGCCACCGACTTGTCTGGGGCAGCAGT	351
CYP52A5B	357	AGCATGAAGAACTTGGGGTGTAAGTACTTGGCGTTCAATGCTGGGGCCCCCGGACTTGTCTGGGGCAGCAGT	426
CYP52A8A	1	ACCCCCACAAGAACAGTGGAATAATGCCAGTCAA-CAAAGAGTGGTGACAGACGAGGGAGAAAAACGCAAG	0
CYP52A8B	233		301
CYP52D4A	1		0

FIG. 15B-I

CYP52A1A	409	TTT	474
CYP52A2A	490	TTT	555
CYP52A2B	305	TTT	370
CYP52A3A	428	TTT	497
CYP52A3B	211	ACT	267
CYP52A5A	352	ACACT	416
CYP52A5B	427	ACACT	491
CYP52A8A	1		0
CYP52A8B	302	CAACAGT	366
CYP52D4A	1	GATGT	58
CYP52A1A	475	-ATGATA	543
CYP52A2A	556	CTTAAAG	624
CYP52A2B	371	CTTAAAG	439
CYP52A3A	498	-TGAGG	556
CYP52A3B	268	---GTG	329
CYP52A5A	417	-CAGCC	484
CYP52A5B	492	-CTGCC	559
CYP52A8A	1		0
CYP52A8B	367	-CATA	435
CYP52A4A	59	-TCTG	127

FIG. 15B-2

CYP52A1A	544	ACATGAAAGTGAAATCCAAA-TACACTACACTCCGGGTATTGTCCCTTCGTTTTACAGATGTCTCATTTGTC	612
CYP52A2A	625	ATATAAAGTTACTTCGGA-----TATCATTTGTAATCGTGC GTGTCGCAATTGGATGATTTGGAA	683
CYP52A2B	440	ATATAAAGTTATTTTCGGAAC-TCATA---TATCATTTGTAATCGTGC GTGTCGCAATTGGTAAATTTGAAA	505
CYP52A3A	567	AATAATAGTGAACCTTTGTG-TAATAAATCTTCATGCAAGACTTGCATAATTCGAGCTTGGGAGTTTCACG	635
CYP52A3B	330	GATGGTGTGGTTTCTACAA-TGCAAGGGCACAGTTGAAGGTTTCCACATAACGT-TGCACCATATCAAC	397
CYP52A5A	485	TGT--AAAGCTTTATAAGGA-TGTAACGGTAGATGGATAGTTGTGTAGGAGGCGGAGATAAATTAGAT	551
CYP52A5B	560	TGT--AAAGTTTCACAAGGA-TCTAGATGGATATGTA-AGGTGTGTAGGAGGAGCGGAGATAAATTAGAT	625
CYP52A8A	1		0
CYP52A8B	436	CCA--ATAAGACTATCCCTT-CTTACAACCAAGTTTCTGCCCGCCCTGTCTGGCA-ACAGATGCTGGCC	501
CYP52D4A	128	GATATCTGCCAAGGTATATAGCAGAACGTGCTGATGGTTCTCCGGTCATATTCTGTGTGGTAGTTCTGCA	197

FIG. 15B-3

CYP52A1A	613	TTACTTTT	682	AGGTCATAGG	AGTTGCCTGTGAGAGATC	ACAGAGATTATC	CACACTCACATTTATCGTAGTT
CYP52A2A	684	CTGCGCTTGA	749	ACCGATTTCATG	CACGAAGCGGAGA-TAA	AAGATTACGT---	AATTATCTCCTGAGACA
CYP52A2B	506	CTGTAGTTGG	565	AACGGATTTCATG	CACGATGGGAGA-TAAC	ACG-----	AGATTATCTCCTAAGACA
CYP52A3A	636	C--CAATTTG	697	ACCTCGTTTCATG	TATGATAAAGAAAGCC	AAAAGGTAAATT--	AGCAGACGC---AATGGG
CYP52A3B	398	T--CAATTTA	462	TATCCTCATTCATG	TATAAAGAGAGCC	AAAAGGTAAATT--	GGCAGACCCCCCAAGGGG
CYP52A5A	552	TTGATTTTG---	617	TGTAAGTTTTG	GATGTCAACCTACT	CCGCACTTTCATGCA-	GTGTGTGTGACACAAGG
CYP52A5B	626	TTGATTTTG---	685	TGTAAAGTTT	AGCTAGCACGTC	AAAGCTACTCCGCACTTTGT---	GTGTAGGGAGCACACA---
CYP52A8A	1		0				
CYP52A8B	502	GACACACTT---	567	TCAACTGAGTTT	GGTCTAGAAATCTT	TGCACATGCACGACA-	AGGAAACTCTTACAAAG
CYP52D4A	198	GGTAAATTTG	266	GATGTCAGGTAGT	GGAGGAGGTTTGT	ATCGGTTGTGTT-TT	CTTCTCCTCTCTCTG
CYP52A1A	683	TCCTATCTCA	750	TGCTGTGTCCT	GTGGTTTCATGAGTTT	TGGATT--	GTTGTACATTAAAGGAATCGCT
CYP52A2A	750	ATTTTAGCCG	816	TGTTTCACACG	CCCTTCTTTGTT-CT	GAGCGAAGGAT--	AAATAATTAGACTTCCACAGCT
CYP52A2B	566	ATTTGGCCTC	628	ATTTCACACG	CCCTTCTT-----	CTGAGCTAAGGAT--	AAATAATTAGACTTCCACAAAGTT
CYP52A3A	698	AACATGGAGT	766	GGAAAGCAATG	GAAAGCACGCC-AG	GACGGAGTAATTT	AGTCCACATACATCTGGGGT
CYP52A3B	463	AACACGGAGT	531	AGTAGAAAGCA	ATGGAAACACGCC-AT	GACAGTGCCATTT	AGCCCAACACATCTAGTATT
CYP52A5A	618	GTGTACTACG	681	TGCGTGTGCG	CCCAAGAGACA---G	CCCAAGGGG--	TGGTAGTGT-GTGTGGCCGAA
CYP52A5B	686	---TACTCCG	741	TCGTCGCTGT	GCGCCAGAGACG---	GCCAGGGG-----	TAGTGT-GTGGTGGTGAA
CYP52A8A	1	GAATTCTTTG	62	GATCTAAATCC	CT---TTGCTAAT	CCCT--	TATCAACGTAAGTTGTGATCATT
CYP52A8B	568	--ACAACAC	630	TTGTGCTGTG	ATGCCACTTGATC---	TTGCTAAGCCT--	TATCAACGTAATGAGATCATT
CYP52D4A	267	ATTCAACCTC	334	CACGTCCTTC	CGGTTCTGTGTCT	GTGAGTC--	GTA

FIG. 15C-I

CYP52A1A	751	GGAAAGCAAGCTAACTAAATTTCTTTGTCAAGGTACACTAACTGTAAAACTTCACTGCCACGCCAG	820
CYP52A2A	817	CATTCTAATTTCCGT--CACGCGAATATTGAA-----GGGGGTACATGTGGCGCTGAA-	869
CYP52A2B	629	CATTAAATATCCGT--CACGCGAANAACGTCAACAATAAGGAAGGGGGGGGTAGACGTAGCCGATGAA-	694
CYP52A3A	767	-----TTTTTTTGTGCGCAAGTACACACCTGGACT-TTAGTTTTTGTCCCCATAAAGTTAACAATCTAA-	830
CYP52A3B	532	CTTTTTTTTTTTTGTGCGCAGGTGCACACCTGGACT-TTAGTTATTGCCCCATAAAGTTAACAATCTCA-	599
CYP52A5A	682	GTGCATGTGACACA--ACGCGTGGGTTCTGCGCAATGTTGGACTAAAGTGCAGGTAAGCAGGACCTGAA	748
CYP52A5B	742	GTGCATGTGACACA--ATACCTGTGTTCTGCGCAATGTTGGGATTTAGTGTAGGTAAGCTGCGACCTGAA	808
CYP52A8A	63	GTTTGTCTGAATTAT-ACACACCAGTGGGAAGAAATATGTTCTAAATTTGCACGTCCTCCACTGGCATTTGTG--	128
CYP52A8B	631	GTTTGTCTGAATTAT-ACACACCAGTGGGAAGAACTGTGTTCTAAATCTGCACGCTCATGGGCATTTGTG--	696
CYP52D4A	335	GCATGTGTGAAAAAAGTAGCGCTTATTTAGACAACCAAGTTCGTTGGGCGGGTATCAGAAAATAGTCTGT	404
CYP52A1A	821	TCCTTTCTGATTGGGCAAGTGCACAAACTACA-ACCTGCAAAACAG-----CACTCCGCTTGTCAACAGTT	885
CYP52A2A	870	-TGTGGGG--CAGTAAACGCAGTCTCTC-----CTCTCCAGGAATAGTCAACCG	918
CYP52ACB	695	-TGTGGGTGCCAGTAAACGCAGTCTCTCTCCCCCCCCCCCCCCCCCTCAGGAATAGTCAACCG	763
CYP52A3A	831	-CCTTTGGC-TCTCCAACTCTCTCCGCCCCCAATATTCGTTTTT-ACACCTCAAGCTAGCGACAGCAC	897
CYP52A3B	600	-CCTTTGGC-TCTCCAGTGTCTCCGCTCCAGATGCTCGTTTT-ACACCTCGAGCTAACGACAAACAC	665
CYP52A5A	749	ACATTCCTCAACGCTTAAGACACTGTTGG-TAGAGATGCGGACCAGG-----CTATTCTTGTCTGT-GCTA	811
CYP52A5B	809	ACACTCCTCAACGCTTGAGACACTGTTGGGTAGAGATGCGGGCCAGGA--GGCTATTCTTGTCTGT-GCTA	875
CYP52A8A	129	-TGTTT-----GTGGGGGGGGGGGTGCACACATTTTAGTGCCA-----TTCTTTGTTGATTAC-CCCT	187
CYP52A8B	697	-TGTTT--GGGGGGGGGGGGGGGTGCACACATTTTAGTGCGAATGTTTGTGTTGCTGGTTCC-CCCT	762
CYP52D4A	405	GTGCACGACCATGAGTATGCAACTTGACGAGCGTCTTAGGA-----ATCCACAGAAATGATAGCAGGAA	469

FIG. 15C-2

CYP52A1A	886	GTCTCCTCTCAACCAACAAAAAATAAGATTAAACTTTTCTTTGCTCATGCATCAATCGGAGTTATCTCTG	955
CYP52A2A	919	AGGAAGGATAACGGATAGAAAGCGGAATGCGAGGAAAAAT--TTTGAACGCGCAAGAAAAAGCAATATCCGG	986
CYP52A2B	764	GGGAAGGATAACGGATAGCAAGTGGAATGCGAGGAAAAAT--TTTGAATGCGCAAGGAAAGCAATATCCGG	831
CYP52A3A	898	AACACCCATTAGAGGGAATGGGGCAAAAGTTAAACACTTTTGGCTTCAATGATTCCTATTCCGTACTACATT	967
CYP52A3B	666	AACACCCATGAGGGGAATGGG-CAAAGTTAAACACTTTTGGTTTCAATGATTCCTATTGCTACT-----	729
CYP52A5A	812	CCCGCGCATGGA-AAATCAACTGCGGGAAGAA--TAAATTATCCGTAGAATCCACAGAGCG-----G	872
CYP52A5B	876	CCCG-TGCACGGA-AAATCGATTGAGGGAAGAA--CAAATTTATCCGTGAAATCCACAGAGCG-----G	935
CYP52A8A	188	CCCCCTATCAT---TCATTCCACACAGGATTAG--TTTTTTCCTCACTGGAAATTCGCTGTCC-----	244
CYP52A8B	763	CCCCCTCCCCCTATCATGCCCCACAGGATTAG--TTTTTTCCTCACTGGAAATTCGCTGTCC-----	822
CYP52D4A	470	GCTTACTACGTGAGAGATTCTCTGCTTAGAGGATG--TTCTCTTCTTGTGATTCCATTAGGTGGGTATCAT	537

FIG. 15C-3

CYP52A1A	956	A--AAGAGTTGCCCTTTGTGTAAATGTGTCCAAA-CTCAAACTGCAAAATAACACAGAAATGAT-----	1016
CYP52A2A	987	GCTACCAGGTTTGTAGCCAGGGAACACACTCCTATTCTGTCTCAATGACTGAACATAGAAAAAA-----	1050
CYP52A2B	832	GCTATCAGGTTTGTAGCCAGGGGACACACTCCT-CTTCTGCACAAAAAATTAACTGACAAAAAA	900
CYP52A3A	968	CTTCTCTTGTGTTTGTGCTTTGAATTGCACCATGTGAATAAAGACAAATTATATATACCTTTTCATC----	1034
CYP52A3B	730	---CTCTTGTGTTTGTGCTTTGCAATTGCAACCATGTGAATAAAGACAAATTATATATACCTTTTCGTC----	793
CYP52A5A	873	A--TAAATTTGCCCACTTCCATCATCAACCACG-CCGCCACTAACTACATCACTCCCTATTT-----	933
CYP52A5B	936	A--TAAATTTGTACATTTGCTGCGTTGCCAC-----CCACAGCATTC-----	978
CYP52A8A	245	-----ACCTGTCAACCCCCCCCCCCCCCCC-CCACTGCC--CTACCTGCCCTGC-----	293
CYP52A8B	823	-----ACCTGTCAACCCCCCTCAC-----TGCCCTGCCCTGC-----	853
CYP52D4A	538	CTCCGGTGGTGACAACTTGACACAAGCAGTTCCGAGAACCCACCAACAATCACCATTCCAGC-----	601
*			
CYP52A1A	1017	TTCCCTCACAATTATATAAACTCACCACATTTCCACAGACCGTAATTTTCATGTCTCAC-TTTCTCTTTT	1085
CYP52A2A	1051	-----CACCAGACGCAATGAACGCACATGGACATTTAGACCTCCCCACATGTGATAGTTTGTCTTAAC	1115
CYP52A2B	901	AATCCACCAAGACACAAATGAATCGCACATGGACATTTAGACCTCCCCACATGTGAAAGCTTCTCTGGCG	970
CYP52A3A	1035	CCTCCTCCTATATCTCTTTTGTGCTAC-ATTTTGTGTTTTCGTTTCTTGTGCTTTTGCACCTCTCCCACTCCC	1103
CYP52A3B	794	TGTCTCCAATGTCTCTTTTGTGCTGCCATTTTGTCTTTTGTCTTTTGTGCTCTCTCCCACTCCC	863
CYP52A5A	934	CTCTCTCTCTCTTTTGTCTTACTCCGCTCCGTTTCCCTTAGCCACAGATACACACCACT-GCAACACAGCA	1002
CYP52A5B	979	TTTTCTCTCTCTTTTGTCTTACTCCGCTCCTGTTTCCCTTATCCAGAAATACACACCACTCATATAAAGAT	1048
CYP52A8A	294	CCTGCACGTCCTGTGTTTGTGCTGTGCTTTTCCACGCTATAAAAGCCCCGTGGCGTCCGGCCAAGGTTT	363
CYP52A8B	854	CCTGCACGCCCCGTGTTTGTGCTGTGTCACCTCCACGCTATAAAAGCCCCGTGGCGTACGGCCAAGGTTT	923
CYP52D4A	602	TATCACTTCTACATGTCAACCTACGATGTATCTCATCACCATCTAGTTTCTTGGCAATCGTTTATTGTT	671

FIG. 15D-I

CYP52A1A	1086	GCTCTTCTTTTACTTAGTCAGGTTTGATAACTTCCTTTTATTATTACCCCTATCTTATTATTATTATTATTC	1155
CYP52A2A	1116	AGA-----AAAGTATAATAAGAACCCATGCCGTCCTTTTCTTTTCGCCGCTTCAACCTTTTCTTTT	1179
CYP52A2B	971	AAAGCAAAAAAGTATAATAAGGACCCATGCCCTTCCCTCTTCTGGGCGGTTTCAACCTTTTCTTTTCT	1040
CYP52A3A	1104	ACAA-----AGAAAAAATAAAGGACCCATGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1146
CYP52A3B	864	ACAATCAGTCGCAACACACAAAGAAAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	933
CYP52A5A	1003	GCA--ACAATTATAAGATACGCC-----AGGCCACCTTCTTTTCTTCTTCTTCTTCTTCTTCTTCT	1064
CYP52A5B	1049	ACG--CTAGCCAGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1110
CYP52A8A	364	TCCACCCAGCCAAAAAACAAGTCTAAAAAATTTGGTTGATCCTTTTGGTTGCAAGGTTTT--CCAC-C	429
CYP52A8B	924	TCCTCACAGCCAAAAAA-----AATTGGCTGATCCTTTTGGGCTGCAAGGTTTTTTCACCCAC-C	982
CYP52D4A	672	ATGGGTCAACATCCAATACAACCTCCACCAA--TGAAGAAGAAAAACGGAAAGCAGAATACCAGAATGACA	739
		*	
CYP52A1A	1156	ATTATACCAACCAACC--AACCATGGCCACACAAGAAATCATCGATTCTGTACTTCCGTACTTGACCAA	1223
CYP52A2A	1180	TCTT-----ACACACATCACGACCA-TGACTGTACACGATATTATCGCCACATACTTCAACCAA	1236
CYP52A2B	1041	TTGTCTATCAACACACACACACCTCACGACCA-TGACTGCACAGGATATTATCGCCACATACATCACCAA	1109
CYP52A3A	1147	GCCC-----AAGAGGTTCTCGCTACCACTAGTCCTTACATCGAGTACTTCTTGACA-ACTACACCAG	1208
CYP52A3B	934	GCTC-----AGGAGGTTCTCGCTACCACTAGTCCTTACATCGAGTACTTCTTGACA-ACTACACCAG	995
CYP52A5A	1065	ACTTCTACAATCCACCAACAGCCACCAACAGCCGCTATGATTTGAACAACCTCTAGAAATTT-----	1127
CYP52A5B	1111	ACTTCTACAACC-----ACCACCAACCAACCAACCAATGATTTGAACAACCTCTAGAAATTT-----	1166
CYP52A8A	430	ACCACCTCCACCA--CCTCAA CTATTGGAACAA--AAGATGCTCGATCAGATCTTACATTACT-----	488
CYP52A8B	983	ACCACCAACCA--CCTCAACTATTCAAAACAA--AGGATGCTCGACCAAGATCTTCCATTACT-----	1041
CYP52D4A	740	GTGTG---AGTTCCTGACCATTTGCTAATCTA-TGGCTATATCTAGTTTGTCTATCGTGGGATG-----	797
		*	

FIG. 15D-2

CYP52A1A	1224	ATGGTACACTGTGATTACTGCAGCAGTATTAGTCTTCTTATCTCCACAAACATCAAGAACTACGTCAAG	1293
CYP52A2A	1237	ATGGTACGTGATAGTACCACCTCGCTTTGATTGCTTATAGAGTCCCTCGACTACTTCTATGGCAGATACTTG	1306
CYP52A2B	1110	ATGGTACGTGATAGTACCACCTCGCTTTGATTGCTTATAGGGTCCCTCGACTACTTTTACGGCAGATACTTG	1179
CYP52A3A	1209	ATGGTACTACTTCATACCTTTGGTGCTTCTTTTCGTTGAACTTTATAAGTTTGCTCCACACAAGGTACTTG	1278
CYP52A3B	996	ATGGTACTACTTCATCCCTTTGGTGCTTCTTTTCGTTGAACTTTCATCAGCTTGCTCCACACAAGTACTTG	1065
CYP52A5A	1128	--GGTATGTCGTTGTGCCAGTGTGTACATCATCAAAACAACCTCCTTGCATACACAAGACTCGCGTCTTG	1195
CYP52A5B	1167	--GGTATATTGTTGTGCCCTGTGTGTACATCATCAAAACAACCTCCTTGCATACACAAGACTCGCGTCTTG	1234
CYP52A8A	489	--GGTACATTGTCTTGCCATTGTTGGCCATTATCAACCAGATCGTGGCTCATGTCAGGACCAATTATTG	556
CYP52A8B	1042	--GGTACATTGTCTTGCCATTGTTGGTCATTATCAAGCAGATCGTGGCTCATGCCAGGACCAATTATTG	1109
CYP52D4A	798	-TGATCTGTGTCGTCTTTCATTTCGCTTGTGTTTATTTTCGGGTAT-GAATATTGTTTATACTAAATACCTTG	865
		* * *	

FIG. 15D-3

CYP52A1A	1294	GCAAAAGAAATTGAAATGTGTGATCCACCATACTTGAAGGATGCCCCGCTCTCACTGGTATTCTGTCTTTGA	1363
CYP52A2A	1307	ATGTACAAGCTTGGTGTAACCATTTTTCAGAAACAGACAGACGGCTGTTTCGGATTCAAAGCTCCGC	1376
CYP52A2B	1180	ATGTACAAGCTTGGTGTAACCGTTTTCAGAAACAAACAGACGGTTATTTCGGATTCAAAGCTCCAC	1249
CYP52A3A	1279	GAAAGCAGGTTCCACGCCAAGCCACTCGGTAACCTTGTTCAGGACCCCTACGTTTGGTATCGTACTCCGT	1348
CYP52A3B	1066	GAAAGCAGGTTCCACGCCAAGCCGCTCGGTAACCTGTTGGATCCCTACGTTTGGTATCGTACTCCGT	1135
CYP52A5A	1196	ATGAAAAGTTGGGTGCTGCTCCAGTCACAAAACAGTTGTACGACACGCTTTCGGTATCGTCAATGGAT	1265
CYP52A5B	1235	ATGAAACAGTTGGGTGCTGCTCCCAATCACAAACAGTTGTACGACACGCTTTCGGTATCGTCAACGGAT	1304
CYP52A8A	557	ATGAAGAAATTGGGTGCTAAGCCATTACACACACGTCACAAACGTTGGGCTTCAAATTCGGCC	626
CYP52A8B	1110	ATGAAGAAATTGGGCGCTAAGCCATTACACACATGTCCAACTAGACGGGTGGTTTGGCTTCAAATTTGGCC	1179
CYP52D4A	866	ATGCACAAACATGGCGCTCGAGAAATCGAGAAATGTGATCAACGATGGGTCTTTGGGTTCGGCTTACCTT	935

CYP52A1A	1364	TCGCGCCCATCAAGGCCAAAGAACGACGGTAG-ATTGGCTAACTTTGCC-----GATGAAGTTT-----	1421
CYP52A2A	1377	TTGAATTGTTGAAGAAGAGAGCGGTAC-CCTCATAGACTTCACA-----CTCCAGCGTATC---C	1436
CYP52A2B	1250	TTGAATTGTTAAAAAAGAGAGTGACGGTAC-CCTCATAGACTTCACT-----CTCGAGCGTATC---C	1309
CYP52A3A	1349	TGCTTTTGATCTACTTGAAGTCGAAAGGTAC-GGTTCATGAAGTTTGCTTGGGCTCTGGAAACAACAAGT	1417
CYP52A3B	1136	TGATCTTGATCTACTTAAAGTCGAAAGGTAC-AGTCATGAAGTTTGCCTGGAGCTTCTGGAAACAACAAGT	1204
CYP52A5A	1266	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGGCTCAAGAGTACAACG-----ATTACAAGTTTG-----	1325
CYP52A5B	1305	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGGCTCAAGAGTACAACG-----ATCACAAGTTTG-----	1364
CYP52A8A	627	GTGAATTCCTCAAAGCAAAAAGTGCTGGGAG-ACTGGTTGATTAAATC-----ATCTCCCGTTT-----	684
CYP52A8B	1180	GTGAATTCCTCAAAGCTAAAAGTGCTGGGAG-GCAGGTTGATTAAATC-----ATCTCCCGTTT-----	1237
CYP52D4A	936	TGCTACTCATGCGAGCCAGCAATGAGGGCCG-ACTTATCGAGTTCAGT-----GTCAAGAGATTCGAGT	998

FIG. 15E-1

CYP52A1A	1422	-----CGACGAGTACCCAAACCACACCTTCTACTTGTCTGTTGCCGGTGCTTTGAAGATTGTGCTGACTGT	1487
CYP52A2A	1437	ACGATCTCGATCGTCCCGATATCCCAACTTTCACATTCGCCGGTCTTTTCCATCAACCTTGTCAATACCCCT	1506
CYP52A2B	1310	AAGCGCTCAATCGTCCAGATATCCCAACTTTTACATTCCTCAATCTTTTCCATCAACCTTATCAGCACCCCT	1379
CYP52A3A	1418	ACATCGTCAGAGACCCCAAGTACAAGACAACTGGGCTCAGGATTGTTGGCCTCCCATTTGATTGAACCCAT	1487
CYP52A3B	1205	ACATTGTCAAAGACCCCAAGTACAAGACCACTGGCTTAGAATTGTCGGCCTCCCATTTGATTGAACCCAT	1274
CYP52A5A	1326	ACCACTCCAAGAACCCCAAGCTGGGCACCTACGTCAGTATTCTTTTCGGCACCAAGATTGTCGTGACCAA	1395
CYP52A5B	1365	ACAGCTCCAAGAACCCCAAGCTGGGCACCTATGTCAGTATTCTTTTTCGGCACCAAGATTGTCGTGACCAA	1434
CYP52A8A	685	-----CCACGA-----TAATGAGGACACTTTCTCCAGCTATGCTTTTGGCAACCAATGTGGTGTTCACCAG	744
CYP52A8B	1238	-----CCACGA-----TAATGAGGACACTTTCTCCAGCTATGCTTTTGGCAACCAATGTGGTGTTCACCAG	1297
CYP52D4A	999	-CGGCGCCACAT--CCACAGAACAAAGACATTGGTCAACCGGGCATTTAGCGGTTCTCTGTGATACTCACCAA	1065
		*	* * *
CYP52A1A	1488	TGACCCAGAAAAACATCAAGGCTGTCTTGGCCACCCCAATTCACTGACTTCTCCTTGGGTACCAGACACGCC	1557
CYP52A2A	1507	TGAGCCGGAGAACATCAAGGCCATCTTGGCCACTCAGTTCAACGATTTCTCCTTGGGTACCAGACACTCG	1576
CYP52A2B	1380	TGAGCCGGAGAACATCAAGGCTATCTTGGCCACCCAGTTCAACGATTTCTCCTTGGGCACCAGACACTCG	1449
CYP52A3A	1488	GGACCCAGAGAACATCAAGGCTGTTTGGCTACTCAGTTCAATGATTTCTCTTTTGGAAACCAGACACGAT	1557
CYP52A3B	1275	AGACCCAGAGAACATCAAAAGCTGTGTGGCTACTCAGTTCAACGATTTCTCCTTGGAAACCAGACACGAT	1344
CYP52A5A	1396	AGATCCAGAGAAATCAAAAGCTATTTTGGCAACCCAGTTTGGTGAATTTTCTTTTGGCAAGAGCACACT	1465
CYP52A5B	1435	GGATCCAGAGAAATCAAAAGCTATTTTGGCAACCCAGTTTGGCGAATTTTCTTTTGGCAAGAGCACGCT	1504
CYP52A8A	745	GGACCCCGAGAAATCAAGGCGCTTTTGGCAACCCAGTTTGGTGAATTTTCTTTTGGCACAGGGTCAAG	814
CYP52A8B	1298	GGACCCCGAGAAATCAAGGCGCTTTTGGCAACCCAGTTTGGTGAATTTTCTTTTGGCAAGAGGGTCAAA	1367
CYP52D4A	1066	GGACCCAGTGAATATCAAAAGCGATGCTATCGACCCAGTTTGATGACTTTTCCCTTGGGTTGAGACTACAC	1135
		** ** *	** ** *

FIG. 15E-2

CYP52A1A	1628	TGTTGAGACCA	CAGATT	TGCTAGAGACC	AGATTGGACAC	CGTTAAAGCCTT	GGAAACCA	CACACAT	CCAAAT	CCAT	1697																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A2A	1647	TGTTGAGACCA	CAGATT	TGCCAGAGAA	CAGATT	TTCCACGTC	CAAGTTGTT	GGAGCC	CACACG	TT	1716																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A2B	1520	TGTTGAGACCA	CAGATT	TGCCAGAGAA	CAGATT	TTCCACGTC	CAAGTTGTT	GGAGCC	CACATG	CAGGT	1589																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A3A	1628	TGTTGAGACCA	CAGATT	TGCTAGAGAA	CAGGTT	TTCTACGTC	CAAGTTGTT	GGAGCC	CACGTT	CAGGT	1697																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A3B	1415	TGTTGAGACCA	CAGATT	TGCTAGAGAA	CACAGGTT	TTCCACGTC	CAAGTTGTT	GGAA	CCACACGTT	CAGGT	1484																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A5A	1536	TGTTGAGACCA	CAGATT	TGCCAGAGAA	CAAGTTGCT	TCATGTG	ACGTCGTT	GGAA	CCACAC	TT	1605																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A5B	1575	TGTTGAGACCA	CAGATT	TGCCAGAGAA	CAAGTTGCT	TCATGTG	ACGTCGTT	GGAA	CCACAC	TT	1644																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A8A	885	TGTTGAGACCA	CAGATT	TGCCAGAGAA	CAAGTTGCT	TCATGTG	ACGTCGTT	GGAA	CCACAC	TT	954																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52A8B	1438	TGTTGAGACCA	CAGTTT	TGCCAGAGAG	CAAGTTGCT	TCATGTG	ACGTCGTT	GGAA	CCACAT	TT	1507																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
CYP52D4A	1206	TGTTGCGTCC	CGCAATT	TTGCCAA	AGATCGGG	TTTCTCAT	ATCCTGGAT	CTAGAA	CCGCAT	TTT	1275																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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FIG. 15F-1

CYP52A1A	1768	GACACCGCTACTGAGTTCTTGTGGTGAAATCCGTTCACTCCTTGTTACGATGAAAAAATTGGGCATCCCAA	1837
CYP52A2A	1787	GACTCCGCCACCGAGTTTGTGGTGAAATCCGTTGAGTCCTTGAGAGATGAATCTATCGGCATGTCCA	1856
CYP52A2B	1660	GACTCCGCCACTGAGTTTGTGGTGAAATCCGTTGAGTCCTTGAGAGATGAATCTATTTGGGATGTCCA	1729
CYP52A3A	1768	GACTCCGCCACCGAGTTCTTGTGGTGAGTCTGCTGAATCCTTGAGGGACGAAATCTATTTGGATTGACCC	1837
CYP52A3B	1555	GACTCCGCCACCGAGTTCTTGTGGTGAGTCTGCTGAATCCTTGAGAGACGACTCTGTTGGTTTGACCC	1624
CYP52A5A	1676	GATTCGGCCACGGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAAATCTATTTGGTATCAACC	1745
CYP52A5B	1715	GACTCGGCCACGGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAAATCTATCGGTATCAACC	1784
CYP52A8A	1025	GACTCGGCCACGGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAGGAAATTTGGCTACGACA	1094
CYP52A8B	1578	GATTACGGACGGAGTTCTTATTTGGTGAGTCCGTCGACTCCTTAAAGGACGAGGAAATTTGGCTACGATA	1647
CYP52D4A	1346	GATGTGGCGACGGGGTTTTTGTGGCGAGTCTGTGGGTGCTTGAAGACGAAAGATGCGAGG-----	1408
		** ** * * * * * ** ** ** **	
CYP52A1A	1838	CTCCAAACGAAA--TCCCAGGAAGAGAAAACTTTGCCGCTGCTTTCAACGTTTCCCAACACTACTTGGC	1904
CYP52A2A	1857	TCAATGGGCTTGACTTTGACGGCAAGGCTGGCTTTGCTGATGCTTTTAACTATTTCGCAGAAATTATTGGC	1926
CYP52A2B	1730	TCAATGCACCTGACTTTGACGGCAAGGCTGGCTTTGCTGATGCTTTTAACTACTCGCAGAACTATTGGC	1799
CYP52A3A	1838	CAACCAACCAAGGATTTTCGATGGCAGAAAGAGATTTTCGCTGACGCTTTCAACTATTTCGCAGACTTACCAGGC	1907
CYP52A3B	1625	CAACCAACCAAGGATTTTCGAAGGCAGAGAGATTTTCGCTGACGCTTTCAACTACTCGCAGACTTACCAGGC	1694
CYP52A5A	1746	AAGACGATATAGATTTTGTGCTGGTAGAAAGGACTTTGCTGAGTCTGTTCAACAAAGCCCAGGAATACTTGGC	1315
CYP52A5B	1785	AAGACGATATAGATTTTGTGCTGGTAGAAAGGACTTTGCTGAGTCTGTTCAACAAAGCCCAGGAGTATTGTC	1854
CYP52A8A	1095	CGAAAGACATGT--CTGAAGAAAAGACGCAGATTTGCCGACGCGTTTCAACAAGTCGCAAGTCTACGTGGC	1161
CYP52A8B	1648	CGAAGGACATGG--CTGAAGAAAAGACGCAAAATTTGCCGACGCGTTTCAACAAGTCGCAAGTCTATTGTC	1714
CYP52D4A	1409	-----TTCCTGGAAGCAATTCATGAGTCGCAGAAAGTATTTGGC	1445
		** * * * * * * * * * * * * * * *	

FIG. 15F-2

CYP52A1A	1975	GTCCACCACTTGGCCAAAGTACTTTGTCAACAAGGCCTTGAACTTTACTCCTGAAGAACTCGAAGAGAAAT	2044
CYP52A2A	1997	GTGCACAAGTTTGTGCTGACTACTACGTCAACAAGGCTTTGGACTTGA CGCCTGAA CAATTGGAAAAGGAGG	2066
CYP52A2B	1870	GTGCACAAGTTTGTGCTGACTATTACGTCAAGCAAGGCTTTGGACTTGA CACCTGAA CAATTGGAAAAGCAGG	1939
CYP52A3A	1978	GTGCACAAGTTTGTGCTGACCACTATGTGCAAAAAGGCTTTGGAGTTGA CCGACGATGACTTGCAGAAAACAAG	2047
CYP52A3B	1765	GTGCACAAGTTTGTGCTGACCACTATGTGCAAAAAGGCTTTGGAGTTGA CCGACGATGACTTGCAGAAAACAAG	1834
CYP52A5A	1886	GTGCACAAGTTTCAACCACTACTATGTTTCAGAAAAGCTTTGGATGCTAG CCCCAGAA GAGCTTGAAAAGCAAA	1955
CYP52A5B	1925	GTGCACAAGTTTACCACTACTATGTTTCAGAAAAGCTTTGGATGCTAG CCCCAGAA GAGCTTGAAAAGCAAG	1994
CYP52A8A	1232	GTCCACAAGTTTACCACTACTATGTTTCAGAAAAGCTTTGGATGCTAG CCCCAGAA GAGCTTGAAAAGCAAG	1301
CYP52A8B	1785	GTCCACAAGTTTACCACTACTATGTTTCAGAAAAGCTTTGGATGCTAG CCCCAGAA GAGCTTGAAAAGCAAG	1854
CYP52D4A	1517	GTGCGAAAAGTTCTGCAGCCAGTGTGTCCACAAGGCGTTAGATGTTGCA CCGGAAGACACC-----A	1577
		** * * * * * * * * * * * * * * *	
CYP52A1A	2045	CCAAGTCCGGTTACGTTTCTTGTACGAATTGGTTAAGCAAA CCAGAGATCCAAAGGCTCTTGCAAGATCA	2114
CYP52A2A	2067	ATGGTT-----ATGTGTTTTTTGTACGAATTGGTCAAGCAAA CCAGAGACAAGCAAGTGTGTGAGAGACCA	2130
CYP52A2B	1940	ATGGTT-----ATGTGTTCTTTGTACGAGTTGGTCAAGCAAA CCAGAGACAGGCAAGTGTGTGAGAGACCA	2003
CYP52A3A	2048	ACGGCT-----ATGTGTTCTTTGTACGAGTTGGTAAAGCAAA CCAGAGACCCAAAGGTCTTGAGAGACCA	2111
CYP52A3B	1835	ACGGCT-----ATGTGTTCTTTGTACGAGTTGGTAAAGCAAA CCAGAGACCCAAAGGTCTTGAGAGACCA	1898
CYP52A5A	1956	GTGGGT-----ATGTGTTCTTTGTACGAGCTTGTCAAGCAGACAAGAGACCCCAATGTGTGCGTGACCA	2019
CYP52A5B	1995	GCGGGT-----ATGTGTTCTTTGTATGAGCTTGTCAAGCAGACGAGAGACCCCAAGGTGTGCGTGACCA	2058
CYP52A8A	1302	GCGGGT-----ATGTGTTCTTTGTATGAGCTTGTCAAGCAGACGAGAGACCCCAAGGTGTGCGTGACCA	1365
CYP52A8B	1855	GCGGGT-----ATGTGTTCTTTGTACGAGCTTGCCAAAGCAGACGAAAGACCCCAATGTGTGCGTGACCA	1918
CYP52D4A	1578	GCGAGT-----ACGTGTTTCTCCGCGAGTTGGTCAAAACACACTCGAGATCCCGTTGTTTGTACAAAGACCA	1641
		* * * * * * * * * * * * * * * *	

FIG. 15G-I

CYP52A1A	2115	ATTGTTGAACATTATGGTTGCCGGAAGAGACACCACCTGCCGGTTTGTGTGTCCTTTGCTTTGTTGAATTG	2184
CYP52A2A	2131	ATTGTTGAACATCATGGTTGCTGGTAGAGACACCACCGCCGGTTTGTGTGTCGTTTGTGTTTCTTTGAATTG	2200
CYP52A2B	2004	GTTGTTGAACATCATGGTTGCCGCTAGAGACACCACCGCCGGTTTGTGTGTCGTTTGTGTTTCTTTGAATTG	2073
CYP52A3A	2112	GTTATTGAACATTTTGGTTGCCGCTAGAGACACGACCCCGGTTTGTGTGTCATTTGTTTCTACGAGTTG	2181
CYP52A3B	1899	GTTGTTGAACATTTTGGTTGCCGCTAGAGACACGACCCCGGTTTGTGTGTCGTTTGTGTTCTACGAGTTG	1968
CYP52A5A	2020	GTCTTTGAACATCTTGTGGCCGGAAGAGACACCACCTGCTGGGTTGTTGTGTCGTTTGTGTCCTTTGAGTTG	2089
CYP52A2B	2059	GTCTTTGAACATCTTGTGGCAGGAAGAGACACCACCTGCTGGGTTGTTGTGTCCTTTGCTGTGTTGAGTTG	2128
CYP52A8A	1366	GTCTTTGAACATCTTGTGGCAGGAAGAGACACCACCTGCTGGGTTGTTGTGTCCTTTGCTGTGTTGAGTTG	1435
CYP52A8B	1919	GTCTTTGAACATCTTGTGGCTGGAAGGACACACCACCTGCTGGGTTGTTGTGTCCTTTGCTGTGTTGAGTTG	1998
CYP52D4A	1642	AGCGTTGAACGTCCTTGTGCTGGACGCGACACCACCGCGTCGTTATTATCGTTTGCAACATTTGAGCTA	1711
		***** *	
CYP52A1A	2185	GCTAGACACCCAGAGATGTGGTCCAAGTTGAGAGAGAAATCGAAAGTTAACTTTGGTGTGTTGGTGAAGACT	2254
CYP52A2A	2201	GCCAGAAACCCAGAAGTTACCAACAAGTTGAGAGAGAAATTTGAGGACAAGTTTGGACTCGGTGAGAAATG	2270
CYP52A2B	2074	GCCAGAAACCCAGAGGTGACCAACAAGTTGAGAGAGAAATCGAGGACAAGTTTGGTCTTGGTGAGAAATG	2143
CYP52A3A	2182	TCAAGAAACCCCTGAGGTGTTTGTCTAAGTTGAGAGAGGAGGTGGAATAACAGATTGGAATCGGTGAAGAG	2251
CYP52A3B	1969	TCGAGAAACCCCTGAAGTGTTCCTAAGTTGAGAGAGGAGGTGGAATAACAGATTTGGACTCGGCGAAGAGG	2038
CYP52A5A	2090	GCCAGACACCCAGAGATCTGGGCCAAAGTTGAGAGAGGAAATTTGAACAAACAGTTTGGTCTTTGGAGAAAGCT	2159
CYP52A5B	2129	GCCAGAAACCCACACATCTGGGCCAAAGTTGAGAGAGGAAATTTGAACAGCAGTTTGGTCTTTGGAGAAAGCT	2198
CYP52A8A	1436	GCCAGAAACCCACACATCTGGGCCAAAGTTGAGAGAGGAAATTTGAACAGCAGTTTGGTCTTTGGAGAAAGCT	1505
CYP52A8B	1989	GCCAGGAACCCACACATCTGGGCCAAAGTTGAGAGAGGAAATTTGAATCACACTTTGGGCTGGGTGAGGACT	2058
CYP52D4A	1712	GCCCGGAATGACCACATGTGGAGGAAGCTACGAGGAGGTT-----ATCCTGA---CGATGGGACCG	1771
		* *	

FIG. 15G-2

CYP52A1A	2255	CCGCGGTTGAAGAAATTACCTTCGAAGCCTTGAAGAGATGTGAATACTTGAAGGCTATCCTTTAAACGAAAC	2324
CYP52A2A	2271	CTAGTGTGAAGACATTTCTTTGAGTCGTTGAAGTCCTGTGAATACTTGAAGGCTGTTCTCAACGAAAC	2340
CYP52A2B	2144	CTCGTGTGAAGACATTTCTTTGAGTCGTTGAAGTCATGTGAATACTTGAAGGCTGTTCTCAACGAAAC	2213
CYP52A3A	2252	CTCGTGTGAAGAGATCTCGTTTGAGTCCTTGAAGTCCTTGAGTACTTGAAGGCTGTCAATCAATGAAAC	2321
CYP52A3B	2039	CTCGTGTGAAGAGATCTCTTTTGAGTCCTTGAAGTCCTGTGAGTACTTGAAGGCTGTCAATCAATGAAAC	2108
CYP52A5A	2160	CTCGTGTGAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGCGTTTCTTTAATGAAAC	2229
CYP52A5B	2199	CTCGTGTGAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGCGTTTCTTTAATGAAAC	2268
CYP52A8A	1506	CTCGTGTGAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGGCGCGTGTGAAACGAAAC	1575
CYP52A8B	2059	CTCGTGTGAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGGCGCGTGTGAAACGAAAC	2128
CYP52D4A	1772	TCCAG--TGATGAAATAACCGTGGCCGGGTTGAAGAGTTGCCGTTACCTCAAAGCAATCCTTAAACGAAAC	1839

FIG. 15G-3

FIG. 15H-1

CYP52A1A	2465	CCCACCGTTTGGAAAGAAATACTACGGTAAGGACGCTAACGACTTCAGACCAGAAAGATGGTTTGAACCATC	2534
CYP52A2A	2481	CCCACAGAAACCAGCTGTTTACGGTAAGGACGCTCTTGAGTTTAGACCAGAGAGATGGTTTGAGCCAGA	2550
- CYP52A2B	2354	CCCACAGAAACCAGCTGCTACGGTAAGGACGCTTGAAGTTTAGACCCAGAGAGGTGGTTTGAGCCAGA	2423
CYP52A3A	2462	CCCACAGAGACCCCAAGTATCTACGGTGCCGACGCTGACGCTCTTCAGACCAGAAAGATGGTTTGAACCCAGA	2531
CYP52A3B	2249	CCCACAGAGACCCCAAGTATCTACGGTGCCGACGCTGACGCTCTTCAGACCAGAAAGATGGTTTGAACCCAGA	2318
CYP52A5A	2370	CTCATTTGGACCCCTGTCTATTACGGCCCTGATGCTGCTGAGTTTCAGACCAGAGAGATGGTTTGAACCCATC	2439
CYP52A5B	2409	CCCACCTTAGATCCTGTCTATTATGGCCCTGATGCTGCTGAGTTTCAGACCAGAGAGATGGTTTGAACCCATC	2478
CYP52A8A	1716	CTCAGACAAATCCTGCTTATTATGGCCGCTGCTGCTGAGTTTAGACCCGAAAGATGGTTTGAACCCATC	1785
CYP52A8B	2269	CTCAGACAAATCCTGCTTATTATGGCCGCTGCTGCTGAGTTTAGACCCGAAAGATGGTTTGAACCCATC	2338
CYP52D4A	1980	CACACTTGAAATGAGAAAGGTATATGGGAATGATAGCCATGTGTTTCGACCCGAGAGATGGGCTGCGTTAGA	2049
		* ** *	
CYP52A1A	2535	TACTAAGAAAGTTGGGCTGGGCTTATGTTCCATTCAACGGTGGTCCAGAGATCTGCTTGGGTCAACAATTC	2604
CYP52A2A	2551	GACAAAGAAAGCTTGGCTGGGCTTCTCCCATTCACCGTGCTCCAGAAATCTGTTTGGGACAGCAGTTT	2620
CYP52A2B	2424	GACAAAGAAAGCTTGGCTGGGCTTCTCCCATTCACCGTGCTCCAGAAATCTGCTTGGGACAGCAGTTT	2493
CYP52A3A	2532	AACTAGAAAGTTGGGCTGGGCATACGTTCCATTCAATGGTGCTCCAGAAATCTGTTTGGGTCAACAGTTT	2601
CYP52A3B	2319	AACTAGAAAGTTGGGCTGGGCATATGTTCCATTCAATGGTGCTCCAGAAATCTGTTTGGGTCAACAGTTT	2388
CYP52A5A	2440	AACCAAAAAGCTCGGCTGGGCTTACTTGCCATTCAACCGTGCTCCAGAAATCTGTTTGGGTCAACAGTTT	2509
CYP52A5B	2479	AACCAAGAAAGCTCGGCTGGGCTTACTTGCCATTCAACCGTGCTCCAGAAATCTGTTTGGGTCAACAGTTT	2548
CYP52A8A	1786	AACCAAGAAAGCTCGGCTGGGCTTCTTGCCATTCAACCGTGCTCCAGAAATCTGTTTGGGTCAACAGTTT	1855
CYP52A8B	2339	AACCAAGAAAGCTCGGCTGGGCTTACTTGCCATTCAACCGTGCTCCAGAAATCTGCTTGGGTCAACAGTTT	2408
CYP52D4A	2050	GGGCAAGAGTTTGGGCTGGTCTGATCTTCCATTCAACGGGCGGCCCGAGAAAGCTGCCCTTGGTCAACAGTTT	2119
		* *	

FIG. 15H-2

CYP52A1A	2605	GCCTTGACTGAAGCTTCTTATGTGATCACTAGATTGGCCAGATGTTTGAAACTGTCTCATCTGATCCAG	2674
CYP52A2A	2621	GCCTTGACAGAAGCTTCGTATGTCACTGTCAAGTTGCTCCAGGAGTTTGACACACTTGTCATGGACCCAG	2690
CYP52A2B	2494	GCCTTGACAGAAGCTTCGTATGTCACTGTCAAGTTGCTCCAAAGAGTTTGACACACTTGTCATGGACCCCA	2563
CYP52A3A	2602	GCCTTGACCGAAGCTTCAATACGTCACTGTCAAGTTGCTCCAGGAGTTTGACACACTTGTCATGGACCCAG	2671
CYP52A3B	2389	GCCTTGACTGAAGCTTCAATACGTCACTGTCAAGTTGCTCCAAAGAGTTTGAAAACTTGTCCCTGGATCCAA	2458
CYP52A5A	2510	GCCTTGACGGAAGCTGGCTATGTGTTAGATTGGTGCAAAGAGTTCTCCACGTTAGGCTGGACCCAG	2579
CYP52A5B	2549	GCCTTGACCGAAGCTGGTTACGTTTGGTCAGATTGGTGCAAAGAGTTCTCCACATTAGGCTGGACCCAG	2618
CYP52A8A	1856	GCCTTGACTGAAGCCGGTTACGTTTGGTTAGACTTGTTCAGGAGTTTCCAAACTTGTCACAAGACCCCG	1925
CYP52A8B	2409	GCCTTGACCGAAGCCGGTTACGTTTGGTTAGACTTGTTCAGGAAATCCCTAGCTTGTCAAGGACCCCG	2478
CYP52D4A	2120	GCAATCCTTGAAGCTTCGTATGTTTGGCTCGATTGACACACAGTGCTACACGACGATACAGCTTAG--AA	2186

FIG. 15H-3

CYP52A1A	2675	GTCTCGAATACCCCTCCACCACCAAGTGATTACACTTGACCATGAGTCACAACGATGGTGTCTTTGTCAAGAT	2744
CYP52A2A	2691	ACACCGAATATCCACCTAAGAAAATGTCGCAATTTGACCATGTGCTTTTCGACGGTGCCAATATTGAGAT	2760
CYP52A2B	2564	ACACCGAATATCCACCTAGGAAAATGTCGCAATTTGACCATGTCCCTTTTCGACGGTGCCAACATTTGAGAT	2633
CYP52A3A	2672	ACACCGAATATCCACCAAAAATTCGAGAACACCTTGACCTTGTGCTCTTTGATGGTGTGCTGATTAGAAT	2741
CYP52A3B	2459	ACGCTGAGTACCCACCAAAAATTCGAGAACACCTTGACCTTGTCACTCTTTGATGGTGTGCTGACGTTAGAAT	2528
CYP52A5A	2580	ACGAGGTGTACCCGCCCAAGAGGTTGACCAACTTGACCATGTGTTTGACGAGATGGTGTCTATTGTCAAAGTT	2649
CYP52A5B	2619	ATGAAGTGTATCCACCAAGAGGTTGACCAACTTGACCATGTGTTTGACGAGATGGTGTCTATTGTCAAAGTT	2688
CYP52A8A	1926	AAACCAAGTACCCACCACTAGATTGGCACACCTTGACGATGTGCTTGTGACGGTGCACACGTCACAAGAT	1995
CYP52A8B	2479	AAACTGAGTACCCACCACTAGATTGGCACACCTTGACGATGTGCTTGTGACGGGGGCATACGTCACAAGAT	2548
CYP52D4A	2187	CTACCGAGTACCCACCAAGAAACTCGTTTCATCTCACGATGAGTCTTCTCAACCGGGGTGTACATCCGGAAC	2256
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CYP52A1A	2745	GTAA-AGTAGTCGATGCTGGGTATTCGATTACATGT--GTATAGGAAGATTTTGGTTTTTTTATTTCGTTCT	2811
CYP52A2A	2761	GTATTAGAGGGTCATGTGTATTATTT-GATTGTTTA-----GTTTGTAATTACTGATTAGGTTAATTCATG	2824
CYP52A2B	2634	GTATTAGAGGATCATGTGTATTATTTTGATTGGTTTAGTCTGTTTGTAGCTATTGATTAGGTTAATTCACG	2703
CYP52A3A	2742	GTAATAAGGTTGCTTTTCCCTTGCTAATTTTCTCTGTATAGCTTGTGTATTTAAATTTGAATCGGCAATTG	2811
CYP52A3B	2529	GTTCTAAGGTTGCTTATCCTTGCTAGTGTATT--TATAGTTTGTGTATTTAAATTTGAATCGGCGATTG	2595
CYP52A5A	2650	TGACTAGCGCGGTGGTGAATGCGTTTGATTTTGTA---GTTTCTGTTTGACGTAATGAGATAACTATTCA	2716
CYP52A5B	2689	TGACTAGTA-CGTA-TGAGTGCGTTTGATTTTGTA---GTTTCTGTTTGACGTAATGAGATAACTATTCA	2753
CYP52A8A	1996	GTCAATAGGTTTCCC---CATACAAGTAGTTCAGTA--ATTATACACTGTTTTTACTTTCTCTTCATACC	2059
CYP52A8B	2549	GCAATAGGTTT-----TGTTTTGACTTTTGTTCATA--	2580
CYP52D4A	2257	TAGAACTTGATTATGTGTATTATGGTTAATCGGGGCAAGCACTGCAAGTCATTGATGTTTGTGGAAGCCC	2326

FIG. 15I-I

CYP52A1A	2812	TTTTTTTAAATTTTGTAAATTAG-TTTAGAGATTTCATTAATACATAGATGGGTGCTATTTCCGAAACT	2880
CYP52A2A	2825	GATTGTTATTTATGTAGAGGGTT-----TGCGGTGTTGCATTCACTTGGGATCGTTCAGGTTG	2885
CYP52A2B	2704	GATTGTTATTTATGTAGGGGTGCGTGTGTGTGTGTGTGATTACATGGGATCGTTCAGGTTG	2773
CYP52A3A	2812	ATTTTCTGTATACCAATAAACCGTA-----GTGCGATTTGACCAAAACCGTTCAAAGTTTTTGTCTC	2873
CYP52A3B	2596	ATTTTCTGTGTACTAATAACTGTA-----GTGGGTTTTCACCAAAACCGTTCAAACCTTTTTTTTTT	2657
CYP52A5A	2717	GATAAGCGAGTGGATGTACGTTT-TGTAAGAGTTT--CCT-TACAACCTTGGTGGG-TGTGTGAGGTT	278
CYP52A5B	2754	GATAAGCGGGTGGATGTACGTTT-TGTAAGAGTTT--CCT-TACAACCTTGGTGGG--TGTGTGAGGTT	2817
CYP52A8A	2060	AAATGGACAAAAAGTTTAAAGCATG-CCTAACAAACGTGACCG-GACAAATTGTGTCCGCACTAGTATGTAAACA	2127
CYP52A8B	2581	-----TGCAAGT	2587
CYP52D4A	2327	AGCATTGGTGTCCGGAGCATCAATAACCAATGTCCTTGAAAGGTTTGATTTTCTTGACCTTCTTCTCT	2396
CYP52A1A	2881	TTACTTCTATCC--CCTGTATCCCTTATTATCCCTCTCAGTCACATGATTGCTGTAAATTGTCGTGCAGGA	2948
CYP52A2A	2886	ATGTTTCTTCCATCCT--GTGAGTCAAAAAGGAGTTTGTGTTTGTAACTCCGGACGATGTTTTTAAATAG	2953
CYP52A2B	2774	TTGTTTCTCTTCCATCCT--GTTGAGTCAAAAAGGAGTTTGTGTTTGTAACTCCGGACGATGCTTAGATAG	2841
CYP52A3A	2874	TCGTTGACG-----TGCTCGTCTATCAGCACTGTTTGAAGACGAAAGA-GAAAAATTTTTTGTGTA	2930
CYP52A3B	2658	TTTTTCTTCCCTACCTTCGTTGCTCGTCTATCAGCACTGTTTGAACGAAAAAGAAAAATTTTTTGTGTA	2727
CYP52A5A	2782	GAGGTTGCATCTT-GGGGAGATTACACCTTTTG-CAGCTCTCCGTATACACTTGTACTCTTTGTAAACCTC	2849
CYP52A5B	2818	G----CATCTTAG-GGAGAGATAGCACCTTTTG-CAGCTCTCCGTATACAGTTTTTACTCTTTGTAAACCTA	2881
CYP52A8A	2128	ATTGTA AAAAATAG-TGTACACTAAATTGTGTGGTGGCGGAGATAAATTACAGTTTGGTTTGTGTAAACCTC	2196
CYP52A8B	2588	AGTTCAGTAAT--TACACACTAAATTGTGTGGTGGCGGCGGATAAATTACCGTTTGGTTTGTGTAAAAAT	2654
CYP52D4A	2397	GAGCTTCTTTCCG--TCAAACTTGATACAGAAATGGCCATCATTTTCAAGGAACAACCA-CGTACGACGGCCGG	2463

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CYP52A1A	2949	CACAACTCCCTAACGGACTTAAACCATAAACAGCTCAGAACCATAGCCGACATCACTCCTTCTTCTC	3018
CYP52A2A	2954	AAGTCGATCTCCATGTGATGTGTTTGACTGTGTTGACTGTTGATTAATGTAATCTGCG-----GACGTTATA	3016
CYP52A2B	2842	AAGTCGATCTCCATGTGATGTGTTT-GACTGCTACTCTGATTAATCTGTAAGCCTAGACGTTATG	2910
CYP52A3A	2931	AACAACACTGTCCAAATTTACCCAAACGTGAACCATTAAG--CAAATGAGCGGCC-----CTTTCAA	2989
CYP52A3B	2728	AACAACATTGCCCAAACCTTACCCAAACGTGAACCATTAACCAATGAGCGGCG-----CTTTCAA	2788
CYP52A5A	2850	TATCAATCATGTGGGGGGGGTTCATTGTTTGGC-CATGGTGGTGCAATGTTAAATCCGCC-AACTACC	2917
CYP52A5B	2882	TGCCAATCATGTGG-----GGATTCAATTGTTGCC-CATGGTGGTGCAATGCAAAATCCCCCAACTACC	2944
CYP52A8A	2197	GCGGATAATCTCTGGC-----AGTTTCTCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2260
CYP52A8B	2655	TCGGACATCTCTGGT-----GGTTTCCCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2718
CYP52D4A	2464	TACCGCATCTGGAGTA---TCTCGCCGTCGTTCAAGTAG--CAGCAAAACAGCAACGACGTCACCATCTG	2528

FIG. 15I-3

CYP52A1A	3019	TCTTCTCCAAACCAATAGCATGGACAGACCCACCCCTCCTATCCGAATCGAAGACCCCTTATTGACTCCATAC	3088
-CYP52A2A	3017	CAAGCATGTGATTGTGGTTTTT-----GCAGCCT-TTTCACGACAAATGATCGTCAGACGATTACGTAA	3079
CYP52A2B	2911	CAAGCATGTGATTGTGGTTTTT-----GCAACCTGTTTGCACGACAAATGATCGACAGTCGATTACGTAA	2975
CYP52A3A	2990	CTGGTCGCTGGAAGCATTCGGG-----GATATCTACAACGCCCTTAAAGTTTGAACAGACATTGATTAG	3054
CYP52A3B	2789	CTGGTCACTGGAGGCATTTCGGG-----GATATCTACAACGCCCTTAAAGTTTGAAGAACATTGATTAG	2853
CYP52A5A	2918	CAATCTCACATGAAACTCAAGCACACTAAAAAAGATGTTGGGGGAAACCTT-TGGTTTCCCTTC	2986
CYP52A5B	2945	CAATCTCACATGAAACTCAAGCACACTAAAAAAGATGTTGGGGGAAACCTT-TTGAATG-----	3005
CYP52A8A	2261	CAAAATCAAAAGGGG-----AGAACTTAAACACCCCTTATCTCTCCACTC-TAGGTTGTAGCT	2318
CYP52A8B	2719	CAAAATCGAAAGGGGGGGGGGAGAAAGTTAAACACCCCTGTTCC--CACCG-TAGGCTGTAGCT	2785
CYP52D4A	2529	CTTCCCAATCTTGACACC-----ACAGATACCCCTGCGGCTTCATGTGATCAAAAACGTGCGGAACC	2590
CYP52A1A	3089	CCACCTGGAAGCCCTCAAGCCACACACGTCATCCAGCCACCCATCACCAACATCCCTCTACTCGACAAC	3158
CYP52A2A	3080	TCTTTGTTA-----GAGGGGTAAATAAAACAAATGGCAGCCAGAAATTTCAAACATTTCTGCAAAACAATG	3144
CYP52A2B	2976	TCCATATTAT-TTAGAGGGGTAAATAAAATAAA-TGGCAGCCAGAAATTTCAAACATTTTGCAAAACAATG	3043
CYP52A3A	3055	ACACCATAGA-TTTCAGCGGCATCAAGAAATGACC-----TTGCCACATTTTGACGACCCCAACACCACTG	3119
CYP52A3B	2854	ACACCATAGA-TTTCAGCGGCATCAAGAAATGACC-----TTGTCCACATTTTGACAAACCCCAACACCACTG	2918
CYP52A5A	2987	TTAGTAATT--AAACACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTCACTCTGGGCTGC	3054
CYP52A5B	3006	TTGGGGAAA--ACTTTCGTTTCTTCTCAGTAATTAACGTTCTCACTCAGACAAACCCACCTGGGCTGC	3073
CYP52A8A	2319	CTTGTGGG--ATGCAATTGTCGTACGTTTTTTTATGTTTGTCTAGACTTTTGTGATTACGTTGGATTTC	2386
CYP52A8B	2786	CTTGTGGGGGATGTAATTGTCGTACGTTTTTC-ATGTTTGGCCCGAGACTTTGATGATTACGTAGGCTTTC	2854
CYP52D4A	2591	CCGGGTATATGTCCATGTAATTCTCCATGGCCACCT--CCATCAACACACTGATGGAGCGACTGACGGTG	2658

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FIG. 15J-I

CYP52A1A	3159	GTCCAAAAGACGGCGAGTTCTGGTGTGCCCCGGAATCAGCCATCCCGGCCACATACAAGCAGCCGTTGATT	3228
CYP52A2A	3145	CAAAAAATGGGAAACTC--CAACAGACAAAA-AAAAAACTCCGCAGCACTCCGAACCCACAGAACAAATG	3211
CYP52A2B	3044	CAAAAGATGAGAACTC--CAACAGAAAAAATAAAAACTCCGCAGCACTCCGAACCCACAAAAACAATG	3111
CYP52A3A	3120	GAAGAAATCAGCCAGA---AACTAGGCGATGGATCCAAGCCTGTGACCTTGCCCAATGGAGACGAAAGTG	3185
CYP52A3B	2919	GAAGAAATCAGCCAGA---AACTAGGCGATGGATCCAAGCCTGTGACCTTGCCCAATGGAGACGAAAGTG	2984
CYP52A5A	3055	AGACAAACAGAAAAAAGAAACAAAATCCAGATAGAAAAACAAAGGGCT-GGACAAACCATAAAT-AAAC	3122
CYP52A5B	3074	AGACAAACAGAAAAA---C-CAAAATCCAGATAGAAAGAAAGGGCT-GGACAAACCATAAAT-AAAC	3135
CYP52A8A	2387	TTATGTCGTAGGGGTG---CTTGAAAGAGTGTCAAAATGTGACAGGCG-ACGCTATTTCGACAT-GAAC	2450
CYP52A8B	2855	TTATGTCGTAGGGGTG---CTTGACACAAAGTGTCAAAAGGTGACAGGCG-ACGTTATTTCGACAT-GAAC	2918
CYP52D4A	2659	CCACCACTGCCCTCGG-----TTGAGTCAAGGCAGTATGATGCCCGGATCCAGTACTCCAATGGGAACC	2722
CYP52A1A	3229	GCGTGCAATCTCGGCGAGCCACAATGGAGCCACGCATTCGGACCATGAAGCAAAGTACATTCAACGAGA	3298
CYP52A2A	3212	GGG---CGCCAGAAATTATGACTATTGTGACTTTTITA-----CGCTAACGCTCATTTGCAGTG	3266
CYP52A2B	3112	GGGG--GCGCCAGAAATTATGACTATTGTGACTTTTTTTT--ATTTTTTCCGTTAACTTTTCATTGCAGTG	3177
CYP52A3A	3186	GAGTTGAACCAAGCGTTCCTAGAAAGTTACCACATTATTGTGCAATGAGTTTGACTTGGACCAATTGAACG	3255
CYP52A3B	2985	GAGTTGAACCAAGCGTTCCTAGAAAGTTACCACATTATTGTGCAACGAGTTTGACTTGGACCAATTGAACG	3054
CYP52A5A	3123	AATCTAGGGTCTACTCCATCTCCACTGTTCTCTCTTCAGACTTAGCT-AAACAAACAACTCACTTCA	3191
CYP52A5B	3136	AACCTAGGGTCCACTCCATCTTTCACT---TCTTCTCTTCAGACTTATCT-AAACAAACGACTCACTTCA	3201
CYP52A8A	2451	GCGAAAAGGGTTATTGTGCATCAATACGAG--GGGCTGACTCTAGTCTAGG--ATGGCAGTCCTAGGTTGC	2515
CYP52A8B	2919	GCAAAAAGGGTAATTGTGCATCGATACGAG--GGGTTGCCCTCTGGTCTAAG--AAGGACCCCCCAGGTTGC	2983
CYP52D4A	2723	TCT-----GCACGGTGTGCTGCTGCAGTTTTTTGAGGCGTATTTCGA-----TCCATGATCGTTCTTTGG	2779

FIG. 15J-2

CYP52A1A	3299	TCACGGGTGTTTCAG-TGTCGCAGATTGAGAAAGTTCGACGATGGATGGAAGTACGATCTCGTTGCGGATT	3367
CYP52A2A	3267	TAGTGCCTTTACACGG-----GGTATTGCTTTCTACAATGCAAGGCCA-CAGTTGAAGGTTTGCACC	3328
CYP52A2B	3178	AAGTGTGTACACGGGTGGTGAATGGTTTCTACAATGCAAGGCCA-CAGTTGAAGGTTTCCACA	3246
CYP52A3A	3256	CGGCAGAGTTGTTATACTA-CGCTGGCGACATATCCTACAAGAAGGGCACATCAATCGCAGACAGTGCCA	3324
CYP52A3B	3055	CGGCCGAGTTGTTATACTA-CGCCGGCGACATATCCTACAAGAAGGGCACATCAATTGCCGACAGTGCCA	3123
CYP52A5A	3192	CCATGGATTACGCAGGCATCAGCGTGGCTCCATCAGAGG-CGAGGCCCTGAAGAACTCG--CAGAATT	3258
CYP52A5B	3202	CCATGGATTACGCAGGTATCAGCGTGGTCCATCAGAGG-CGAAGCCTTGAAGAACTCG--CCGAGTT	3268
CYP52A8A	2516	AAACATGTTGCACCA-TATCCCTCCTGGAGTTGGTCGAC--CTCGCCTACGCC-ACCCTCA--GCGATCG	2579
CYP52A8B	2984	AAACATGTTGCACTG-CATCCCACTCAGAGTTGGTCGAC--CACGCCCTACGCTTACCCCTCA--GCGATCG	3048
CYP52D4A	2780	TGCTGTAGTATAACGAGCT--CTTGGTGTCTTGAAATGGAACAGGTTGGATGTGTTGTGAGTTTGTCT	2847

FIG. 15J-3

CYP52A1A	3368	ACGACTTCGGTGGGTTGTTATCTAAACGAAGATTCTATGAGACGCAGCATGTGTTTCGGTTCGAGGATTC	3437
CYP52A2A	3329	TAACGTTGCCCGTGTCAACTCAATTTGAC-----G--AGTAACCTCCTAAGCTCGAATTATGC	3385
CYP52A2B	3247	TAACGTTGCACCATATCAACTCAATTTATC-----CTCATTATGTGATAAAGAAGAGCCAAA	3305
CYP52A3A	3325	GATTGTCTTATTATTGAGAGCAAACTAC-----ATCTTGAACATACTTGGGTATTTGAT	3379
CYP52A3B	3124	GATTGTCTTACTATTGAGAGCAAACTAC-----ATCTTGAACATACTTGGGTACTTTAT	3178
CYP52A5A	3259	G-ACCATCCAGAACCCAGCCATCCAGCT-----TGAAAGAAATCAACACCGGCATCCAGAAGGACGACTT	3321
CYP52A5B	3269	G-ACCATCCAGAACCCAGCCATCCAGCT-----TGAAAGAAATCAACACCGGCATCCAGAAGGACGACTT	3331
CYP52A8A	2580	GCACTTTCCGTTGTTCAATATTCTC-----CTTCCCATTTGTTCCAGGGGTTA--TC	2629
CYP52A8B	3049	GCACTTTCCGTTGTTCAATATTCTCT-----CCCCCCTGCTTCCCCCCTATGTTCCAGGGATTA--TC	3110
CYP52D4A	2848	GCGTGCTTGGTTTGCAAGTCTTCGATCG-----AGCGTAGTAGTAGACAGTTGGCGGG	2901
CYP52A1A	3438	TGCGTACGTCAATGAGTGTGCCCTTTTGATGGACCCCAAGGAGGAGTTACGTGGTTGGGACGTACAGATCC	3507
CYP52A2A	3386	AGCT-CGTGCGTCAACCTATGTGCAGGAAAGAAATAATCCAAAA--AATCGAAA-ATGCGACTTTCGAT	3451
CYP52A2B	3306	AGGT-AAT-TGGCAGACCCCCCAAGGGGAAACCGGAGTAGAAAGC--AATGGAAACACGCCCATGACAGT	3371
CYP52A3A	3380	TTCCG-AAGCAGGGATTGGATTGTATAGTCACGGACAAACGACGCGT--TGTTTGATAGTATTTTGAAAAAGT	3446
CYP52A3B	3179	TTCCG-AAGCAGCGATTGGATGTGATAGTCAACGACAAACGCGT--TGTTTGATAATAATTTTGAAAAAGT	3245
CYP52A5A	3322	TGCC-AAGTTGTTGTCTGCCACCCCGGAAAAATCCCAAGCACA--AGTTGAACGGCAACCCACGAATT-	3387
CYP52A5B	3332	TGCC-AAGTTGTTGTCTGCCACCCCGGAAAAATCCCAAGCACA--AGTTGAATGGCAACCCACGAATT-	3397
CYP52A8A	2630	AACA-ACGTTGCCGGCTCCTC-----CCCAATTA-----CAAGAAAAATAAAATT-	2674
CYP52A8B	3111	AACA-ACGTTGCCGGCTCCTCCTCCCCCCTCCCCCCTTAT-----GTACAAGAAAAATTAAATT-	3171
CYP52D4A	2902	GGTGGTGGCTCGGGCTTTATTCTGTGTTGTGTTCTTCTTAGT--CTTGGAATGACGCTGTATCGAC	2969

FIG. 15K-I

CYP52A1A	3508	ATTGAAAGGTTAGCTGGGTAAAGACGGGACGTGGA-GTGGACCATGG--CGACGACGTGCGATCCT	3573
CYP52A2A	3452	TTTGAATAAACCAAAAAGAAAATGTCGCACTTTTTC-----TCGCTCTCGCTCTCTCGACCCAAATCA	3516
CYP52A2B	3372	GCCATTTAGCCACA--ACACATCTAGTATTCTTTT-----TTTTTTGTGGCAGGTGCACACCTGG	3433
CYP52A3A	3447	TTTGAAGAAGATCTAC-----AAGTTGATAAGCGTGTGA-----ACGATATGATTGACAAAGCAAGGTGA	3507
CYP52A3B	3246	TTTGAAGAAGATCTAC-----AAGTTGATAAGCGCGTTGA-----ACGATATGATTGACAAAGGTGA	3306
CYP52A5A	3388	GTCTGAGGTCGCCATTGCCAAAAGAGTACGAGGTGTGATTGCCTTGAGCGACGCCACAAAAGACCCA	3457
CYP52A5B	3398	GTCCGAAGTCGCCATTGCCAAAAGAGTACGAGGTGTGATTGCCTTGAGCGACGCCACAAAAGAACCA	3467
CYP52A8A	2675	GTGCGACGGCACCGATCTGTCAAAGATACAGATAA-----ACCTTAAATCTGCAAAAACAAGACCCC	2736
CYP52A8B	3172	GTGCGACGGCACCGATACGTCAAAGATACAGAGAA-----ACCTTAA-----TCC	3216
CYP52D4A	2970	GGTTCGTAGTATAAGTAGCGCCAATATGAGAAATGTATA-----TCCGCATCACCCAAAGACTCTTCAGCCT	3034
CYP52A1A	3574	GGTGGGTTTATCCGCA-ATGGATAACTCGATTGAGCA-TCCCTGGAGCAATCGCAAAAGATGTGCCTAG	3641
CYP52A2A	3517	CAACAAATCCTCGCGCGAGTATTTGACGAAAC--CACACAAATAAAAAAACAATTTACACCACT	3584
CYP52A2B	3434	ACTTTAGTTATTGCCC-CATAAAGTTAAACAATCT--CACCTTTGGCTCTCCAGTGTCTCCGCTCCAGA	3500
CYP52A3A	3508	CAAGCGACATCAACAGTCTAGCATTCATCAATTG--CATCAACTACTCGAGAGGTCAACTATTCTCCGCA	3575
CYP52A3B	3307	CAAGCGACATCAACAGTCTAGCATTTATCAACTG--CATCAACTACTCGAGGGGTCAACTATTCTCCGCA	3374
CYP52A5A	3458	ATCAAAGTGACCTCCAGATCAAGATCTTGATTGACAAAGTTCAAGGTGTACTTGT---TTGAGTTGCCCTG	3524
CYP52A5B	3468	ATCAAAGTCACCTCCAGATCAAGATCTTGATTGACAAAGTTCAAGGTGTACTTGT---TTGAGTTGCCCG	3534
CYP52A8A	2737	TCCCCATAGCCTAGAAGCACCCAGCAAGATGATGGAGCAACTCCTCCAGTACTGGTACATCGCACTCTCTG	2806
CYP52A8B	3217	CTCCCCATAGCCTAGAAGCATCAAAAAGATGATTGAGCAACTCCTCCAGTACTGGTACATTCGACTCCCTG	3286
CYP52D4A	3035	GTTACAACGACTGAGGCTGTTGGCCGTGTGACCAATTGGTTTCTTTGGTGACCTAGATTGGTCCCGCAGG	3104

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FIG. 15K-2

CYP52A1A	3642	TG---	TATTAACTACATACAGAAATAAAAACGTGTCTTGATTTCATTGGTTT---	GGTTCCTTGTGGGTT	3705
CYP52A2A	3585	T----	CTTTTCTTCAACAGTCAACAAAAACAACAAATTATACACCATTTCAACGATTTT	TGCTCTTAT	3650
CYP52A2B	3501	TG---	CTCGTTTACACCCCTCGAGCTAACGACAAACACACCCATGAGGGGAATGGG	CAAAGTT----	3562
CYP52A3A	3576	CA---	CGAACTTTTGGG-AC	TGGTTTGGATTGGTCGACATCTATTCAACCAAGTTTGGCACATTA	3641
CYP52A3B	3375	CA---	CGAACTTTTGGG-AC	TGGTTTGGATTGGTTGACAACTATTTCAAACCAAGTTTGGCTCATTA	3440
CYP52A5A	3525	AC---	CAGAAAGTTCTCCTACTCCATCTCCATCGTGTCCTCCGTCAACATCGCCCCC	-TGGACCTTGTCTCGGG	3590
CYP52A5B	3535	AC---	CAGAAAGTTCTCCTACTCCATCGTGTCCTCCGTTCACATTCGCCCCC	-TGGACCTTGTCTCGGTG	3600
CYP52A8A	2807	TA---	TGGTTCATCCTTCGCTACTTGGCTTCCACGACGACGCGTCTACTTG	-CGCCACAAGCTCGGCG	2872
CYP52A8B	3287	TA---	TGGTTCATCCTTCGCTACTTGGCTTCCACGACGACCAACCATCTACTTG	-CGCCACAAGCTCGGCG	3352
CYP52D4A	3105	GAAAGCAAGGCTGCTAGGGGGGCATACCAACAAGGTCGTGTAATCAGTATCTAT	TGCTACCATGTG		3174

FIG. 15K-3

CYP52A1A	3706	CCGAGCCAAATATTTACATCATCTCCTAAATTTCTCCAAGAAATCCCAACGTAGCTAGTCCAGCACGCCCT	3775
CYP52A2A	3651	AAATGCTATATAATGGTTTAAATTCAACTCAGGTATGTTTAT-TTTACTGTTTTCAGCTCAAGTATGT--T	3717
CYP52A2B	3563	AAACACCTTTTGGTTTCAATGATTCCTATTTGCTACTCTCTTGTGTTTGTGTTTGTATTTGCACCATGT--G	3630
CYP52A3A	3642	GACAACTACAAGAAGGTATTTGGCATTGATACCTGAAGAACATCAGCGATGAAGACATCTTGATCATAC--A	3709
CYP52A3B	3441	GACAACTACAAGAAAGTATTTGGCATTGATACCTGAAGAACATCAGTGATGAAGATATCTTGATCGTAC--G	3508
CYP52A5A	3591	AGAAAGTTGACCCACGGGCTTGATCAACTTTGGCCTTCCAGAAACAACAAGCAGCACCTTGGACGAGGTCAAT-G	3659
CYP52A5B	3601	AGAAAGTTGACCCACGGGCTTGATCAACTTTGGCCTTCCAGAAACAACAAGCAGCACCTTGGACGAGGTCAAT-G	3669
CYP52A8A	2873	CGGCGCCATTTCACGCACACCCAGTACGACGGCTGGTATGGGTTCAAGTTTGGGCGGGAGTTTCTCAA--G	2940
CYP52A8B	3353	CGGCGCCGTTTCACGCACACCCAGTACGACGGATGGTATGGGTTCAAGTTTGGGCGGGAGTTTCTCAA--G	3420
CYP52D4A	3175	TGTGGTTGGGGGAAATTTCCCGCATTTTGTGTAAACGAAAGTTCTAGAAAAGTTCTCGTGGGTTCTGAG-A	3243
CYP52A1A	3776	CTGAGATCTTATTAAATATCGACTTCTCAACCACCGGTGGAATC--CCGTTCAGACCATTTGTTACCTGTA	3843
CYP52A2A	3718	CAAACTACTAACTACTTTTGTATGTTTGTGCTTTTCTAGAAATCAAAAACAACGCCCAACAACGCCGAGCTT	3787
CYP52A2B	3631	AAATAAACGACAAATTATATATACCTTT--TCGTCTGTCTC---CAATGTCT-CTTTTGTGCTGCCATT	3692
CYP52A3A	3710	CTTCTCTCCATCGACACTACAAATTGTTTAAAGCTGGTGTGGACAA-GAAAAGACGACGCTGCAGTTGAACA	3778
CYP52A3B	3509	CTTCTCTCCATCGACACTACAAATTGTTTAAAGCTGGTGTGGATAA-GAAAAGACGACGCCACTGTTGACCA	3557
CYP52A5A	3660	ACATCTTCAACGAGTTTCATCGACAAAGTTCTTTTGGCAACACGGAG--CCGCAATTGAC-----CAACTTCT	3722
CYP52A5B	3670	ACATCTTCAACGAGTTTCATCGACAAAGTTCTTTTGGCAACACAGAG--CCGCAATTGAC-----CAACTTCT	3732
CYP52A8A	2941	GCGAAGAAAGATCGGGCGGCAGACGGACTTGGTGCAATGCGCGGTT--CCGTGGCGG-----CATGGACA	3001
CYP52A8B	3421	GCGAAGAAAGATTTGGAAGGCAGACGGACTTGGTGCAATGCGCGGTT--CCGTGGAGGGGG-----CATGGATA	3484
CYP52D4A	3244	ATCTGCTGGAACCATCCACCCGCATTTCCTGTTGCCAAAGTGGGAA-GAGCAATCAACCCACCCCTGCTTTG	3312

FIG. 15L-1

CYP52A1A	3844	GTGTGTTTGCTTGTCTTGTGATGACAAATGATGTATTTGTACGATACCTGAAATAATAAAACATCCAGT	3913
CYP52A2A	3788	GTGGAATAGACGGTTTGTCTTACTCATTAGATGGTCCAGATTACTTTTCAAGCCAAAGTCTCT - CGAGTT	3856
CYP52A2B	3693	TTGCTTTTGTCTTTTGTCTTTTGCACT - - CTCTCCCACTCCCAATCAGTGCAGCAACACA - CAA	3755
CYP52A3A	3779	GTTCACAAGTACATCACTTCAACAGT - - GTACGAGACTACAACTCCAACATCGGCTCCACAGCCAAAG	3846
CYP52A3B	3578	GTTCACAAGTACATCACTCAACAGT - - GTCGCAAGACTACAACTCCAACATCGGAGCCACAGCCAAAG	3645
CYP52A5A	3723	TGACCTTGTGCGGTGTGTGGACGGTTGATTGACCATGCC - AACTTCTTGAGCGTGTCTTCGCGGACCT	3791
CYP52A5B	3733	TGACCTTGTGCGGTGTGTGGACGGTTGATTGACCATGCC - AACTTCTTGAGCGTGTCTTCAGGACCT	3801
CYP52A8A	3002	CCTTCTCGAGCTACACTTTCGGCATCCATATCATCTCTTACC - CGGACCCCGGAGAACATCAAGCGGTCT	3070
CYP52A8B	3485	CTTCTCGAGCTATACTTTCGGCATCCATATCATCTCTTACT - CGGACCCCGGAGAACATCAAGCGGTCT	3553
CYP52D4A	3313	CCCAATCAGCCATTCCCCTGGGAATATAAATTCAAC	3348
CYP52A1A	3914	CATTGAGCTTATTACTCGTGAACTTATGAAAGAACTCATTCAGCCGTTCCCAAAAACCCAGAAATTGAA	3983
CYP52A2A	3857	TTGTTTGCTGTTTCCCCCAATTCTTAACATGAAAGGTTTTTATAAGGTCCAAAGACCCCAAGGCATAGTT	3926
CYP52A2B	3756	ATGATATCGATTTGTCCAAAACCAAACCTCAGTGGCTTTGAGGTGTTGACGAGTT	3755
CYP52A3A	3847	ATGATATCGATTTGTCCAAAAGCC	3900
CYP52A3B	3646	TCAAGATCTTCTTGAACTTTGGACTCGTATGTGGAC	3663
CYP52A5A	3792	TCAAGATCTTCTTGAACTTTGGACTCGTATGAGCAAACTCGGACTTCTTGAACGACGTGGAGAACTACTC	3826
CYP52A5B	3802	TGGCGACGCAGTTCGATGACTTCTCGCTCGGTGGCAGGATCAGGTTCTTGAAGCCGTTGTTGGGTATGG	3871
CYP52A8A	3071	TGGCGACGCAGTTCGATGACTTCTCGCTCGGTGGCAGGATCAGGTTCTTGAAGCCGTTGTTGGGTATGG	3140
DYP52A8B	3554	TGGCGACGCAGTTCGATGACTTTTTCG	3579
CYP52D4A	3349		3348

FIG. 15L-2

CYP52A1A	3984	GATCTTGCTCAACTGGTCA	4053
CYP52A2A	3927	TCATGCAAGTAGTAGATCGCCATGATCTGATAC	3948
CYP52A2B	3756	TTTCTTGGTTCCTTCTTGTGCTG	3755
CYP52A3A	3901		3900
CYP52A3B	3669		3668
CYP52A5A	3827		3826
CYP52A5B	3872	CGACTTTTGTACGACGAGCCGAAACGAGTACCAGAACTT	3910
CYP52A8A	3141	GATATTCACGTT	3152
CYP52A8B	3580		3579
CYP52D4A	3349		3348

FIG. 15L-3

CYP52A1A	4054	AGTTCCTCCACGTACGGCAAGTACGGCAACGAGCTCTGGAAGCTTTGTTGTTGGGGTCATA	4115
CYP52A2A	3949		3948
CYP52A2B	3756		3755
CYP52A3A	3901		3900
CYP52A3B	3669		3668
CYP52A5A	3827		3826
CYP52A5B	3911		3910
CYP52A8A	3153		3152
CYP52A8B	3580		3579
CYP52D4A	3349		3348

FIG. 15M

CYP52A1A	1	MATQEI	IDS	VPYL	-----TKWY	TVITAA	VLFL	STNI	KNYV	38		
CYP52A2A	1	MTVHDI	IATY	-----FTKW	VIVPLA	LIAY	RVL	DYFY	GRY	35		
CYP52A2B	1	MTAQDI	IATY	-----ITKW	VIVPLA	LIAY	RVL	DYFY	GRY	35		
CYP52A3A	1	MSSSPS	FAQ	EVLA	TTSPY	IEYFL	DNYR	WYFI	PLVLLS	FNIS	50	
CYP52A3B	1	MSSSPS	FAQ	EVLA	TTSPY	IEYFL	DNYR	WYFI	PLVLLS	FNIS	50	
CYP52A5A	1	MIEQL	LEY	-----WYVV	VPVLYI	IKQL	LAY	TKTRV		30		
CYP52A5B	1	MIEQI	LEY	-----WYIV	VPVLYI	IKQL	IAY	SKTRV		30		
CYP52A8A	1	MLDQI	LHY	-----WYIV	PLLA	INQI	VAH	VRTNY		30		
CYP52A8B	1	MLDQI	FHY	-----WYIV	PLLV	IKQI	VAH	ARTNY		30		
CYP52D4A	1	MAISS	LLSW	D-----VICV	VFICV	CVYF	GVEY	CYTKY		32		
CYP52A1A	39	KAKKLK	CVDP	PPYL	KDAG	LGTG	ILSL	IAAI	KAKND	GRLANFAD	85	
CYP52A2A	36	LMYKLG	AKP	FFQK	QTDG	CFGK	APLE	LLKK	KS	DGTLIDFTL	82	
CYP52A2B	36	LMYKLG	AKP	FFQK	QTDG	YFGK	APLE	LLKK	KS	DGTLIDFTL	82	
CYP52A3A	51	LERRFH	AKPL	GNFVR	DPTFG	IATP	LLLI	YLKS	GTVM	KFAWGLWNNKYIV	100	
CYP52A3B	51	LERRFH	AKPL	GNVVL	DPTFG	IATP	LLLI	YLKS	GTVM	KFAWSFWNNKYIV	100	
CYP52A5A	31	LMKKLG	AAPV	TNKL	YDN	AFGI	VNGW	KALQ	FKKE	GRAQ	EYND	77
CYP52A5B	31	LMKQLG	AAPV	TNQL	YDN	VFGI	VNGW	KALQ	FKKE	GRAQ	EYND	77
CYP52A8A	31	LMKKLG	AKP	FTHV	QRD	GWLG	FKFG	REFL	KAKS	AGRL	VDLI	77
CYP52A8B	31	LMKKLG	AKP	FTHV	QLD	GWFG	FKFG	REFL	KAKS	AGRL	VDLI	77
CYP52D4A	33	LMHKHG	AREI	ENVIN	DGFF	GFGR	PLPL	LLMR	ASNE	GRLLIEFSV	79	

FIG. 16A-I

[illegible]

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FIG. 16A-2

CYP52A1A	184	KTFDIQELFFRFTVDTATEFLFGESVHSLYDEKLGITP-NEIPGRENFA	232
CYP52A2A	183	KTFDIQELFFRFTVDSATEFLFGESVESLRDESIGMSINALDFDGKAGFA	232
CYP52A2B	183	KTFDIQELFFRFTVDSATEFLFGESVESLRDESIGMSINALDFDGKAGFA	232
CYP52A3A	201	QTFDIQELFFRFTVDSATEFLFGESAESLRDESIGLTPTTKDFDGRRDFA	250
CYP52A3B	201	QTFDIQELFFRFTVDSATEFLFGESAESLRDDSVGLTPTTKDFEGRGDFA	250
CYP52A5A	178	EYFDIQELFFRFTVDSATEFLFGESVHSLKDESIGINQDDIDFAGRKDFA	227
CYP52A5B	178	EYFDIQELFFRFTVDSATEFLFGESVHSLKDEETIGINQDDIDFAGRKDFA	227
CYP52A8A	174	EYFDIQELFFRFTVDSATEFLFGESVHSLKDEEIGYDTKDMSEERRR-FA	222
CYP52A8B	174	EYFDIQELFFRFTVDSATEFLFGESVHSLRDEEIGYDTKDMAEERRK-FA	222
CYP52D4A	180	DYFDIQELYFRFSMDVATGFLFGESVGSLKDE-----D-----ARFL	216
		***** . . . * * * * * * * * * *	
			*
CYP52A1A	233	AAFNVSQHYLATRSYSQTFYFLTNPKEFRDCNAKVHHLAKYFVNKALNFT	282
CYP52A2A	233	DAFNYSQNYLASRAVMQQLYWVLNGKKFKECNKVHKKFADYYVNKALDLT	282
CYP52A2B	233	DAFNYSQNYLASRAVMQQLYWVLNGKKFKECNKVHKKFADYYVSKALDLT	282
CYP52A3A	251	DAFNYSQTYQAYRFLIQQMYWILNGSEFRKSIKVHKKFADHYVQKALELT	300
CYP52A3B	251	DAFNYSQTYQAYRFLIQQMYWILNGAEFRKSIKVHKKFADHYVQKALELT	300
CYP52A5A	228	ESFNKAQEYLAIRTLVQTFYWLNNKEFRDCTKLVKHFTNYVYVQKALDAS	277
CYP52A5B	228	ESFNKAQEYLSIRILVQTFYWLNNKEFRDCTKLVKHRTNYVYVQKALDAT	277
CYP52A8A	223	DAFNKSQVYVATRVVALQNLVWLVNNKEFKECNDIVHKFTNYVYVQKALDAT	272
CYP52A8B	223	DAFNKSQVYLSRVALQTLVWLVNNKEFKECNDIVHKFTNYVYVQKALDAT	272
CYP52D4A	217	EAFNESQKYLATRATLHELFLYFLCDGFRFRQYNKVVRKFCSCVHKALDVA	266
		. . . * * * . . . * * . . . * * * * *	

FIG. 16B-I

CYP52A1A	283	PEELEKSGYVFLYELVKQTRDPKVLQDQLNIMVAGRDTTAGLLSFA	332
CYP52A2A	283	PEQLE-K-QDGYVFLYELVKQTRDKQVLRDQLNIMVAGRDTTAGLLSFV	330
CYP52A2B	283	PEQLE-K-QDGYVFLYELVKQTRDRQVLRDQLNIMVAGRDTTAGLLSFV	330
CYP52A3A	301	DDDLQ-K-QDGYVFLYELAKQTRDPKVLQDQLNILVAGRDTTAGLLSFV	348
CYP52A3B	301	DDDLQ-K-QDGYVFLYELAKQTRDPKVLQDQLNILVAGRDTTAGLLSFV	348
CYP52A5A	278	PEELE-K-QSGYVFLYELVKQTRDPNVLQDQLNILLAGRDTTAGLLSFA	325
CYP52A5B	278	PEELE-K-QGGYVFLYELVKQTRDPKVLQDQLNILLAGRDTTAGLLSFA	325
CYP52A8A	273	PEELE-K-QGGYVFLYELVKQTRDPKVLQDQLNILLAGRDTTAGLLSFA	320
CYP52A8B	273	PEELE-K-QGGYVFLYELAKQTKDPNVLQDQLNILLAGRDTTAGLLSFA	320
CYP52D4A	267	PEDTS----EYVFLRELVKHTRDPVVLQDQALNVLLAGRDTTASLLSFA	311
		**** ** *.* **.* **.* **.* **.* **.* **.* **.*	
CYP52A1A	333	LFELARHPMWSKLREEIEVNFVGVEDSRVEEITFEALKRCEYLKAILNE	382
CYP52A2A	331	FFELARNPEVTNKLREEIEDKFGLGENASVEDISFESLKSCEYLKAVLNE	380
CYP52A2B	331	FFELARNPEVTNKLREEIEDKFGLGENARVEDISFESLKSCEYLKAVLNE	380
CYP52A3A	349	FYELSRNPEVFAKLREEVENRFGLGEEARVEEISFESLKSCEYLKAVINE	398
CYP52A3B	349	FYELSRNPEVFAKLREEVENRFGLGEEARVEEISFESLKSCEYLKAVINE	398
CYP52A5A	326	VFELARHPEIWAHLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAFNE	375
CYP52A5B	326	VFELARNPHIWAHLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAFNE	375
CYP52A8A	321	VFELARNPHIWAHLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAVLNE	370
CYP52A8B	321	VFELARNPHIWAHLREEIEHSHFGLGEDSRVEEITFESLKRCEYLKAVLNE	370
CYP52D4A	312	TFELARNDHMMWRKLREEVILTMGPSSD---EITVAGLKSCRYLKAILNE	357
		.* *.* *.* **.* **.* **.* **.* **.* **.*	

FIG. 16B-2

CYP52A1A	383	TLRMYPSPVNFRTATRD	432	TTLPRGGGANGTDPIYIPKGSTVAYVVYKTHR
CYP52A2A	381	TLRLYPSVPQNFRTATKNT	430	TTLPRGGKDGSLPVLVRKGQTVIYGVYAAHR
CYP52A2B	381	TLRLYPSVPQNFRTATKNT	430	TTLPRGGKDGSLPVLVRKGQTVMYGVYAAHR
CYP52A3A	399	TLRLYPSVPHNFRVATRN	448	TTLPRGGEDGYSPIVVKKGQVMYTVIATHR
CYP52A3B	399	TLRLYPSVPHNFRVATRN	448	TTLPRGGKDGCSPIVVKKGQVMYTVIGTHR
CYP52A5A	376	TLRIYPSVPRNFRIATKNT	425	TTLPRGGSDGTSPIILIQKEAVSYGINSTHL
CYP52A5B	376	TLRVYPSVPRNFRIATKNT	425	TTLPRGGPDGTQPIILIQKEGVSYGINSTHL
CYP52A8A	371	TLRLHPSVPRNARFAIKDT	420	TTLPRGGPNKGKDPILIRKDEVVQYSISATQT
CYP52A8B	371	TLRLHPSVPRNARFAIKDT	420	TTLPRGGPNKGKDPILIRKNEVVQYSISATQT
CYP52D4A	358	TLRLYPSVPRNARFATRN	407	TTLPRGGPDGSPILIRKGQPVGYFICATHL
		*** *****		*** * * * *
CYP52A1A	433	LEEYVGKDANDFRPERWFEP	482	STKKLGWAYVPFNGGPRVCLGQQFALTEAS
CYP52A2A	431	NPAVYGKDALLEFRPERWFEP	480	PETKKLGWAFLPFNGGPRICLGQQFALTEAS
CYP52A2B	431	NPAVYGKDALLEFRPERWFEP	480	PETKKLGWAFLPFNGGPRICLGQQFALTEAS
CYP52A3A	449	DPSIYGADADVFRPERWFEP	498	PETRKLGWAYVPFNGGPRICLGQQFALTEAS
CYP52A3B	449	DPSIYGADADVFRPERWFEP	498	PETRKLGWAYVPFNGGPRICLGQQFALTEAS
CYP52A5A	426	DPVYGGPDAAEFRRPERWFEP	475	STKKLGWAYLPFNGGPRICLGQQFALTEAG
CYP52A5B	426	DPVYGGPDAAEFRRPERWFEP	475	STKKLGWAYLPFNGGPRICLGQQFALTEAG
CYP52A8A	421	NPAYYGADAAADFRPERWFEP	470	STRNLGWAFLPFNGGPRICLGQQFALTEAG
CYP52A8B	421	NPAYYGADAAADFRPERWFEP	470	STRNLGWAYLPFNGGPRICLGQQFALTEAG
CYP52D4A	408	NEKVYGNDSHVFRPERWAA	457	LEGKSLGWSYLPFNGGPRSCLGQQFAILEAS
		** * *		***** **

FIG. 16C-I

CYP52A1A	483	YVITRLAQMFETVSSDPGLEYPYPKCIHLTMSHNDGVFVKM	523
CYP52A2A	481	YVTVRLQLQFAHLSMDPDTEYPPKMSHLTMSLFDGANIEM	522
CYP52A2B	481	YVTVRLQLQFGLHLSMDPNTEYPPKMSHLTMSLFDGANIEM	522
CYP52A3A	499	YVTVRLQLQFAHLSMDPDTEYPPKLQNTLTLSLFDGADVRY	540
CYP52A3B	499	YVTVRLQLQFGLHLSLDPNAEYPPKLQNTLTLSLFDGADVRF	540
CYP52A5A	476	YVLVRLVQEFSSHVRLDPDEYVPPKRLTNLTMCLODGAIVKFD	517
CYP52A5B	476	YVLVRLVQEFSSHIRLDPDEYVPPKRLTNLTMCLODGAIVKFD	517
CYP52A8A	471	YVLVRLVQEFPNLSQDPETKYPPPRIAHLTMCLFDGAHVKMS	512
CYP52A8B	471	YVLVRLVQEFPSLSQDPETKYPPPRIAHLTMCLFDGAYVKMQ	512
CYP52D4A	458	YVLARLTQCYTTIQLR-TTEYPPKKLVHLTMSLLNGVYIRTRT	499
		** ** *	*

[illegible]

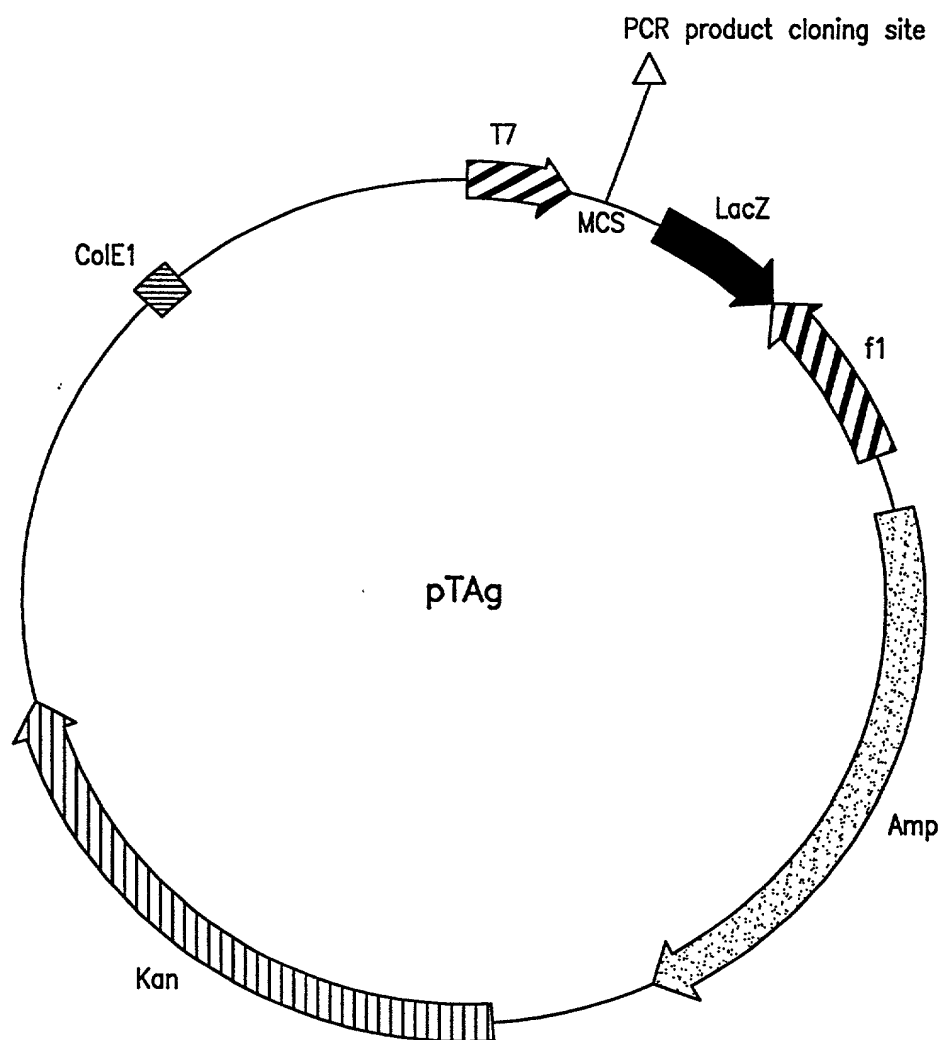


FIG. 17

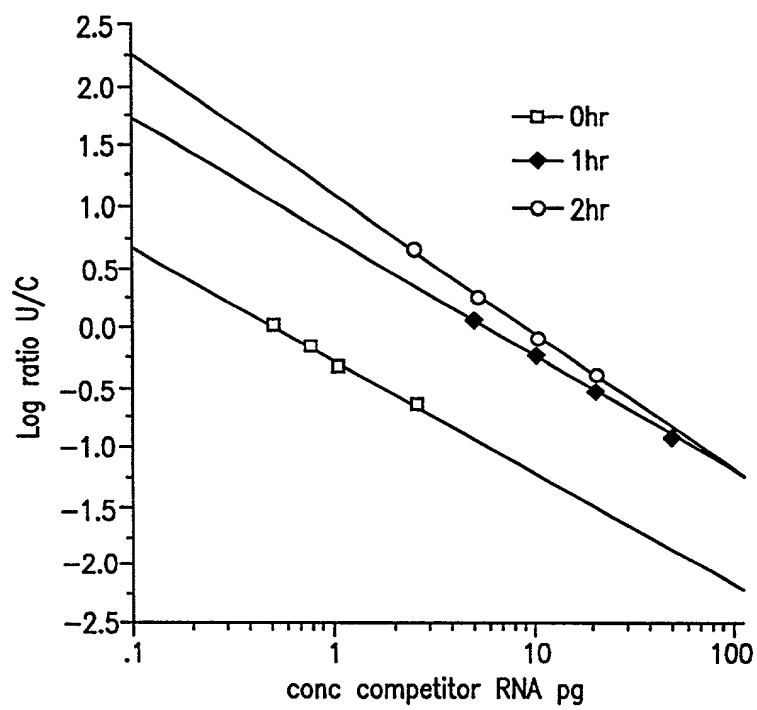


FIG. 18

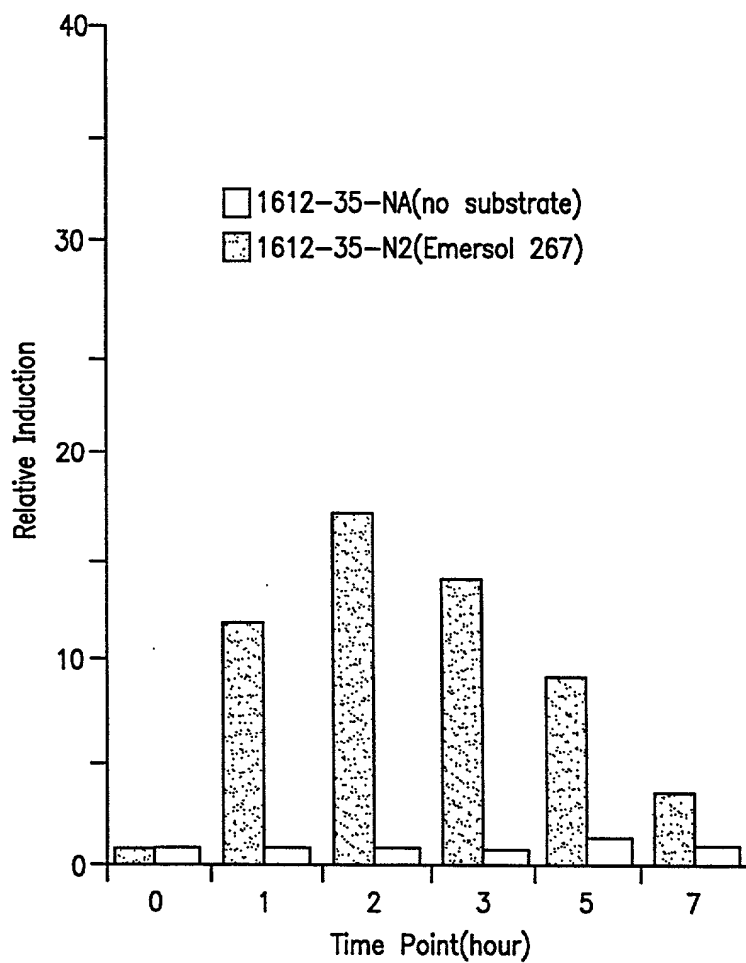


FIG. 19

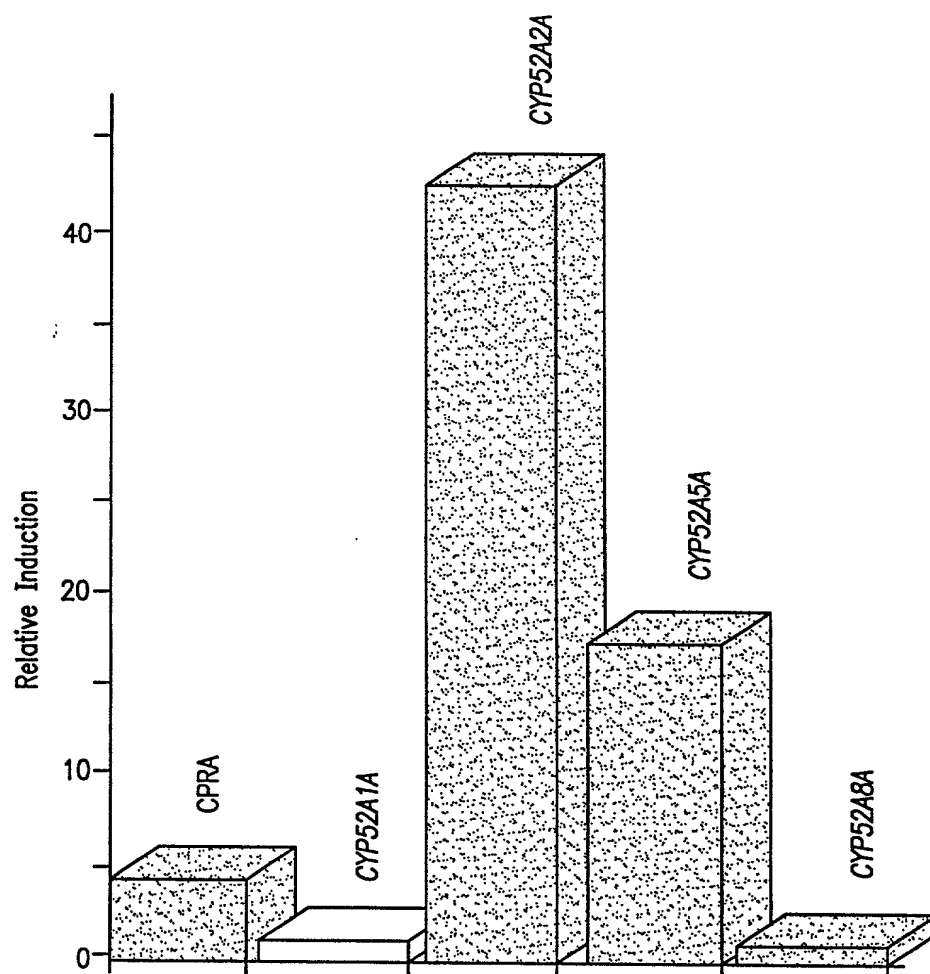


FIG. 20

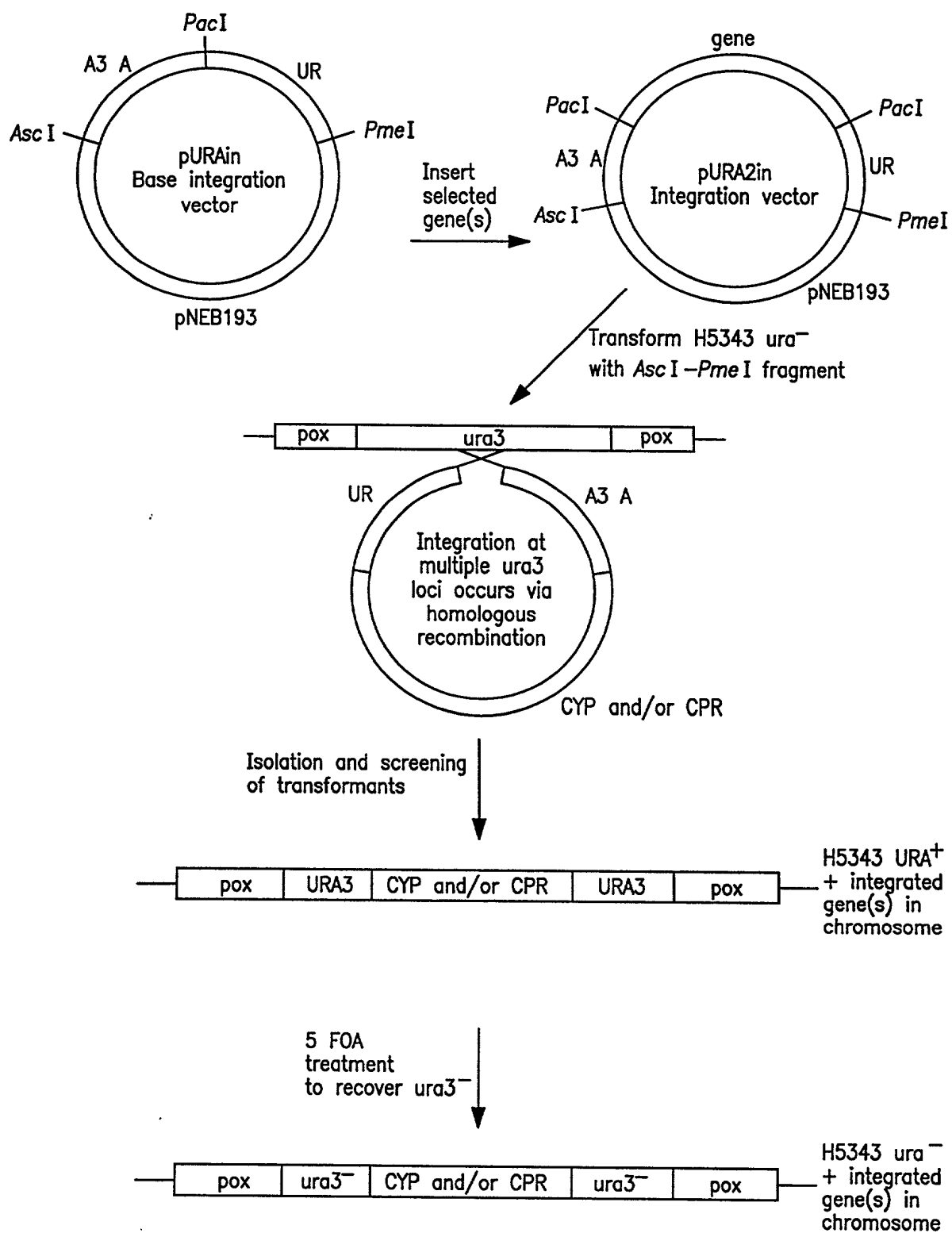


FIG. 2I

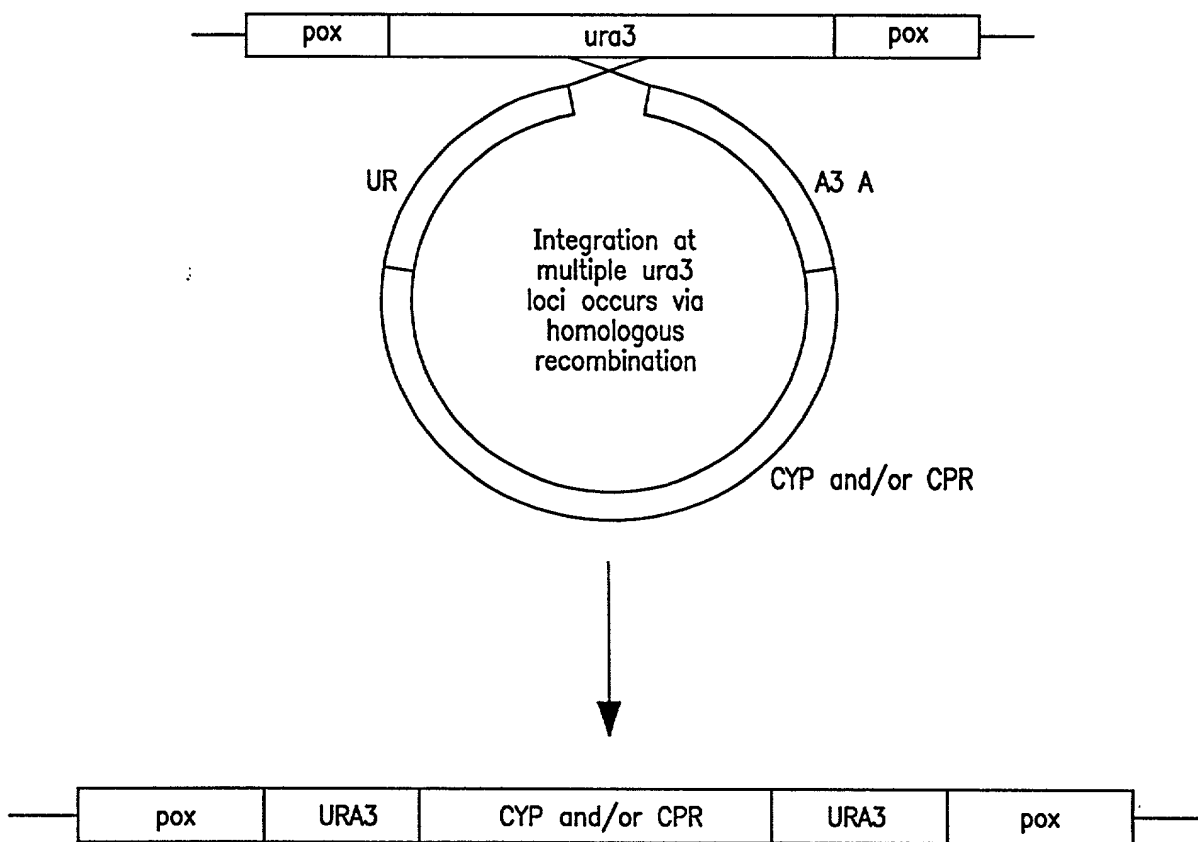


FIG. 22

Sequence Range: 1 to 1712

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10      20      30      40      50      60      70      80
GGTACCGAGC TCACGAGTTT TGGGATTTC GAGTTTGGAT TGTTCCTTT GTTGATTGAA TTGACGAAAC CAGAGGTTTT

90      100     110     120     130     140     150     160
CAAGACAGAT AAGATTGGGT TTATCAAAAC GCAGTTTGAA ATATTCCAGT TGGTTTCCAA GATATCTTGA AGAAGATTGA

170     180     190     200     210     220     230     240
CGATTTGAAA TTTGAAGAAG TGGAGAAGAT CTGGTTTGGA TTGTTGGAGA ATTTCAAGAA TCTCAAGATT TACTCTAACG

250     260     270     280     290     300     310     320
ACGGGTACAA CGAGAAATTGT ATTGAATTGA TCAAGAACAT GATCTTGGTG TTACAGAACA TCAAGTTCTT GGACCAGACT

330     340     350     360     370     380     390     400
GAGAATGCCA CAGATATACA AGCGTCATG TGATAAAATG GATGAGATTT ATCCACAAT TGAAGAAAAGA GTTTATGGAA

410     420     430     440     450     460     470     480
AGTGGTCAAC CAGAAAGCTAA ACAGGAAGAA GCAAACGAAG AGGTGAAACA AGAAGAAGAA GGTAATAAAG TATTTTGAT

490     500     510     520     530     540     550     560
TATATAACAA ACAAGTAAG GAATACAGAT TTATACAATA AATTGCCATA CTAGTCACGT GAGATATCTC ATCCATTCCC

570     580     590     600     610     620     630     640
CAACTCCCAA GAAAAAATAA AAGTGAAAAA AAAAAATCAA CCCTTCCCA AACCTCCCA TCATCATCGT CATCAAAACC

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FIG. 23A

650	660	670	680	690	700	710	720
CCAGCTCAAT	TCGCAATGGT	TAGCACAAA	ACATACACAG	AAAGGGCATC	AGCACACCCC	TCCAAGGTTG	CCCAACGTTT
	M V	S I K T	Y T	E R A S	A H P S	K V A Q	R L>
730	740	750	760	770	780	790	800
ATTCCGCTTA	ATGGAGTCCA	AAAAGACCAA	CCTCTGCGCC	TCGATCGACG	TGACCACAAC	CGCCGAGTTC	CTTTCGCTCA
F R L	M E S	K K T N	L C A	S I D V	T T T A	E F L S	L>
810	820	830	840	850	860	870	880
TCGACAAAGCT	CGGTCCCCAC	ATCTGTCTCG	TGAAGACGCA	CATCGATATC	ATCTCAGACT	TCAGCTACGA	GGGCACGATT
I D K L	G P H	I C L V	K T H	I D I I	S D F S	Y E G T	I>
890	900	910	920	930	940	950	960
GAGCCGTTGC	TTGTGCTTGC	AGAGCGCCAC	GGGTTCCTGA	TATTCGAGGA	CAGGAAGTTT	GCTGATATCG	GAAACACCCGT
E P L	L V L A	E R H	G F L	I F E D	R K F A	D I G N	T V>
970	980	990	1000	1010	1020	1030	1040
GATGTTGCAG	TACACCTCGG	GGGTATACCG	GATCGCGGCG	TGGAGTGACA	TCACGAAACGC	GCACGGAGTG	ACTGGGAAGG
M L Q	Y T S	G V Y R	I A A	W S D I	T N A H	G V T G	K>
1050	1060	1070	1080	1090	1100	1110	1120
GCGTCGTTGA	AGGGTTGAAA	CGCGGTGCGG	AGGGGGTAGA	AAAGGAAAGG	GGCGTGTGA	TGTTGGCGGA	GTTGTGCGAGT
G V V	E G L K	R G A	E G V E	K E R G	V L M L	A E L S	S>
1130	1140	1150	1160	1170	1180	1190	1200
AAAGGCTCGT	TGGCGCATGG	TGAATATACC	CGTGAGACGA	TCGAGATTGC	GAAGAGTGAT	CGGGAGTTCCG	TGATTGGGTT
K G S	L A H G	E Y T	R E T I	E I A K	S D R E	F V I G	F>

FIG. 23B

1210	1220	1230	1240	1250	1260	1270	1280
CATCGCGCAG	CGGACATGG	GGGTAGAGA	AGAAGGGTTT	GATTGGATCA	TCATGACGCC	TGGTGTGGGG	TTGGATGATA
I A Q	R D M	G G R E	E G F D	W I I M T P	G V G L D D>		
1290	1300	1310	1320	1330	1340	1350	1360
AAGGCGATGC	GTTGGGCCAG	CAGTATAGGA	CTGTTGATGA	GGTGGTTCTG	ACTGGTACCG	ATGTGATTAT	TGTCGGGAGA
K G D A	L G Q	Q Y R T	V D E V	V L T G T D	V I I V G R>		
1370	1380	1390	1400	1410	1420	1430	1440
GGGTTGTTTG	GAAAAGGAAG	AGACCCTGAG	GTGGAGGGAA	AGAGATACAG	GGATGCTGGA	TGGAAGGCAT	ACTTGAAGAG
G L F	G K G R	D P E V	E G K R Y R	D A G W K A	Y L K R>		
1450	1460	1470	1480	1490	1500	1510	1520
AACTGGTCAG	TTAGAATAAA	TATTGTAATA	AATAGGTCTA	TATACATACA	CTAAGCTTCT	AGGACGTCAT	TGTAGTCTTC
T G Q	L E *>						
1530	1540	1550	1560	1570	1580	1590	1600
GAAAGTTGTCT	GCTAGTTTAG	TTCTCATGAT	TTCGAAAACC	AATAACGCAA	TGGATGTAGC	AGGGATGGTG	GTTAGTGCCT
1610	1620	1630	1640	1650	1660	1670	1680
TCCTGACAAA	CCCAGAGTAC	GCCGCCCTCAA	ACCACGTCAC	ATTGCGCCCTT	TGCTTCATCC	GCATCACTTG	CTTGAAGGTA
1690	1700	1710					
TCCACGTACG	AGTTGTAATA	CACCTTGAAG	AA				

FIG. 23C

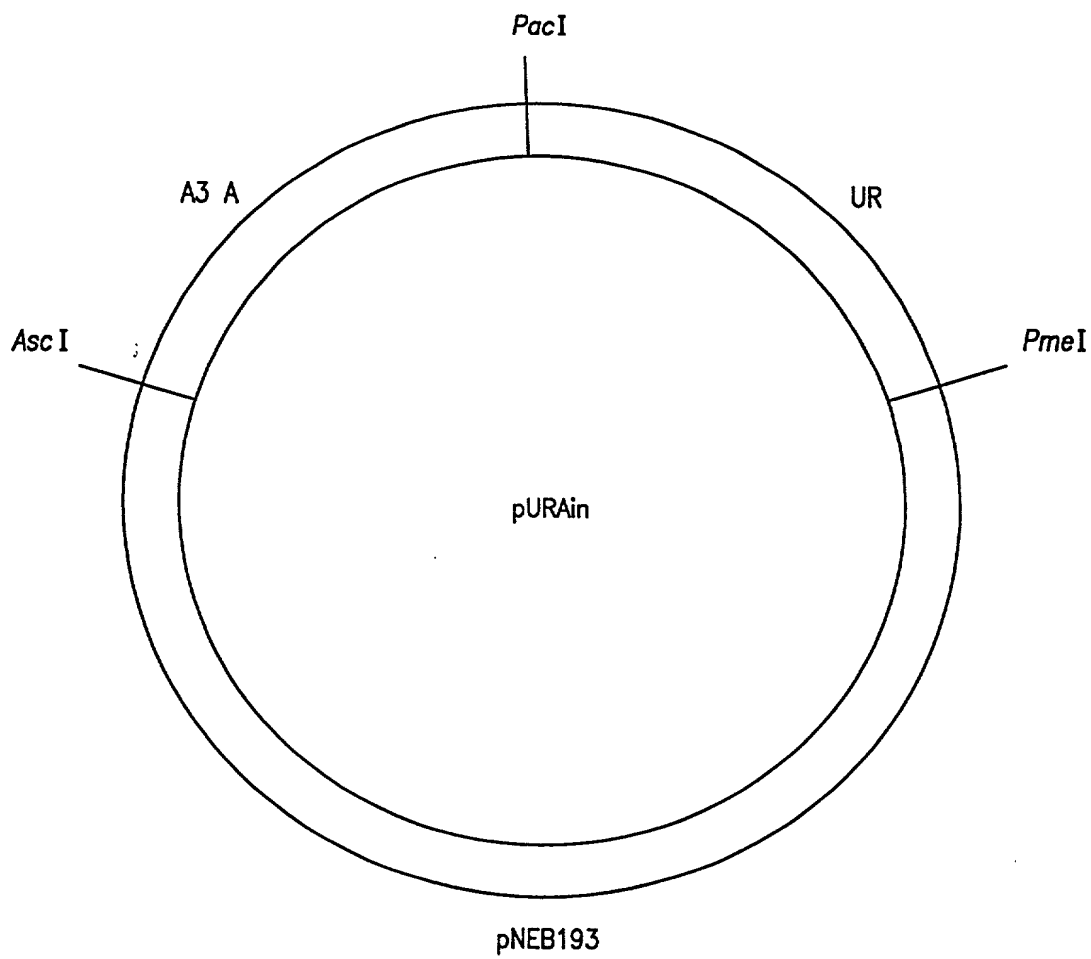


FIG. 24

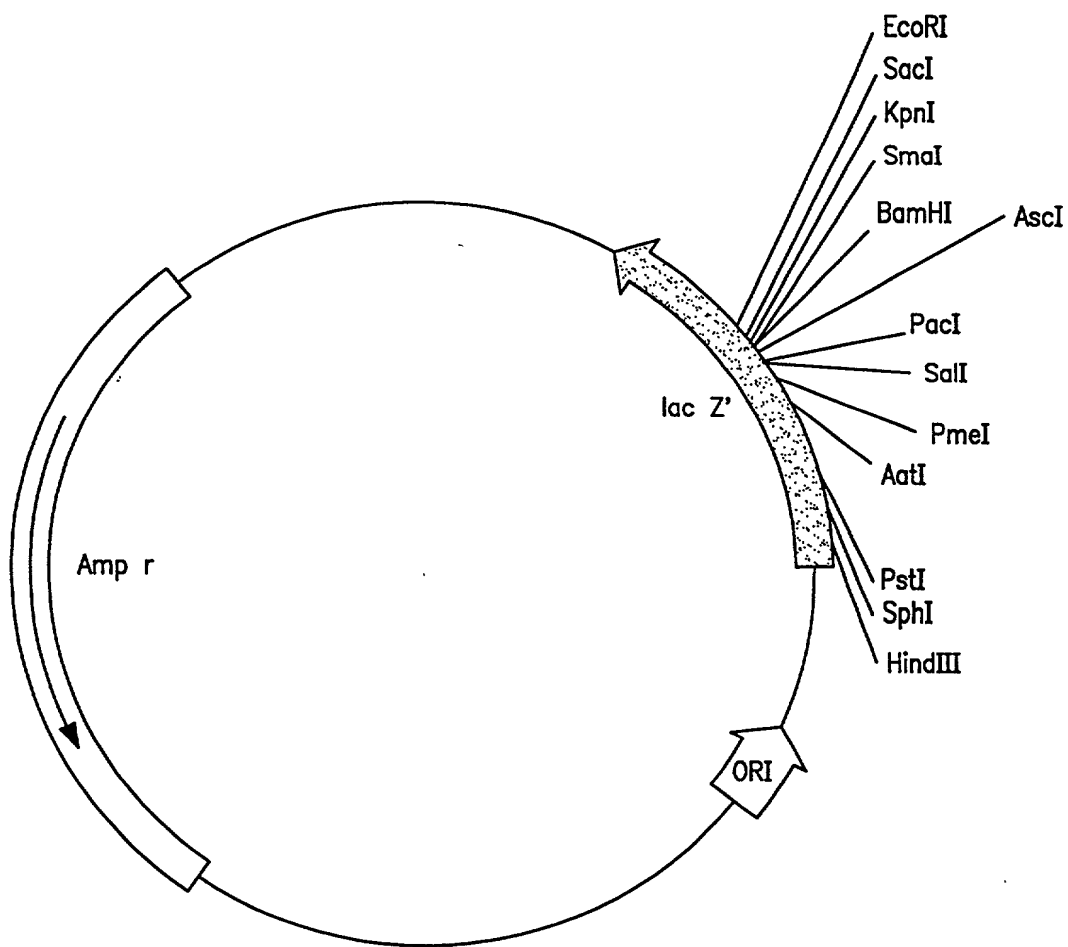


FIG. 25

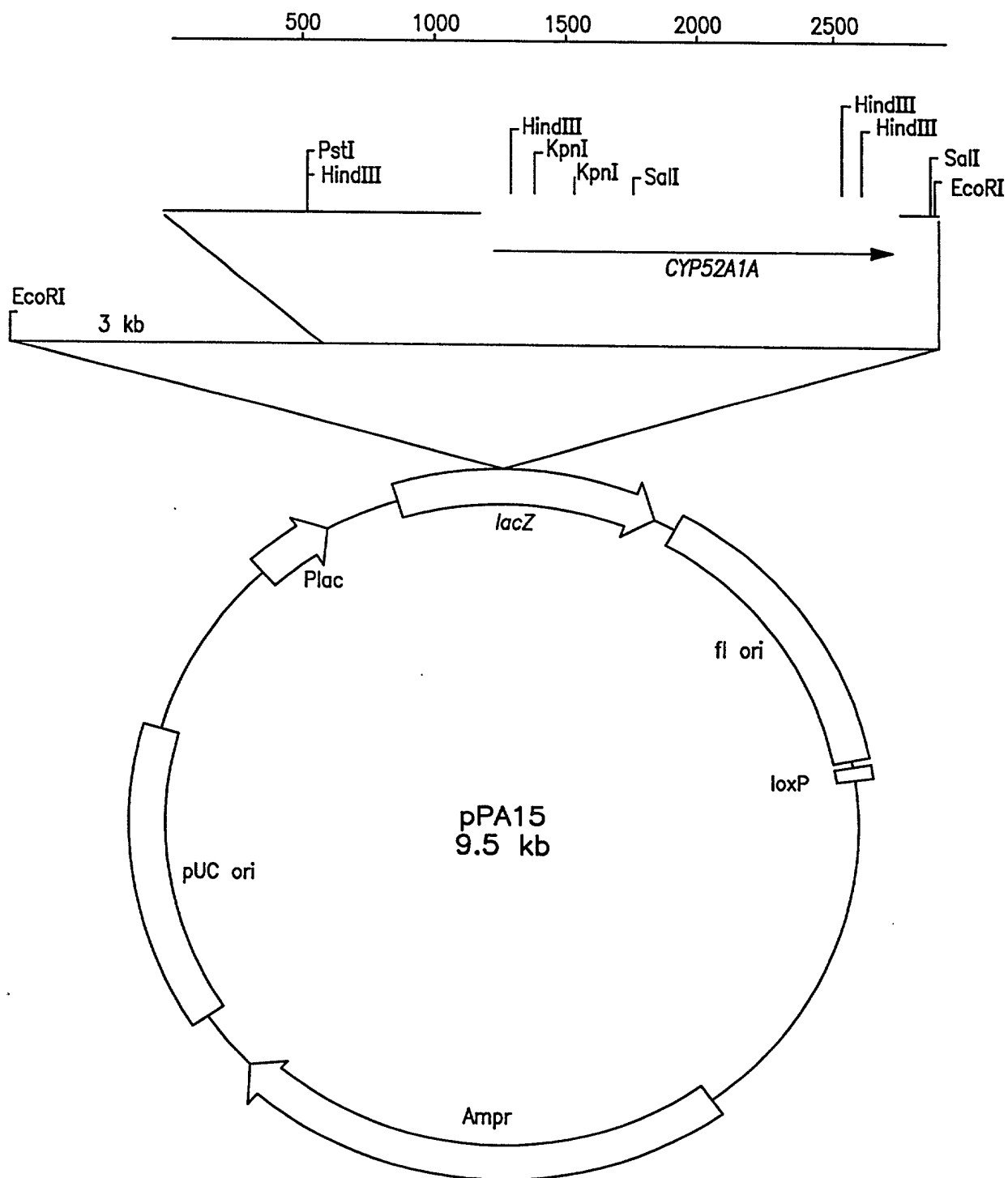


FIG. 26

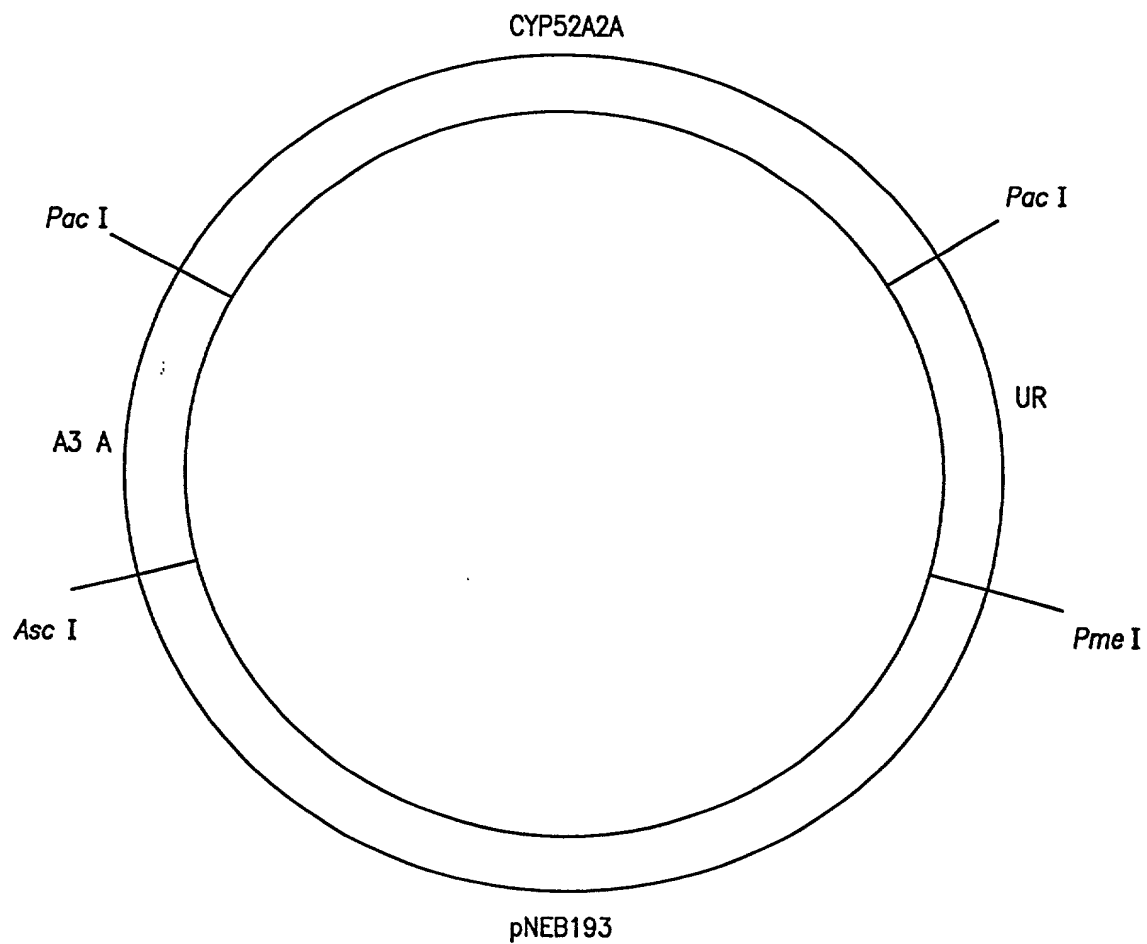


FIG. 27

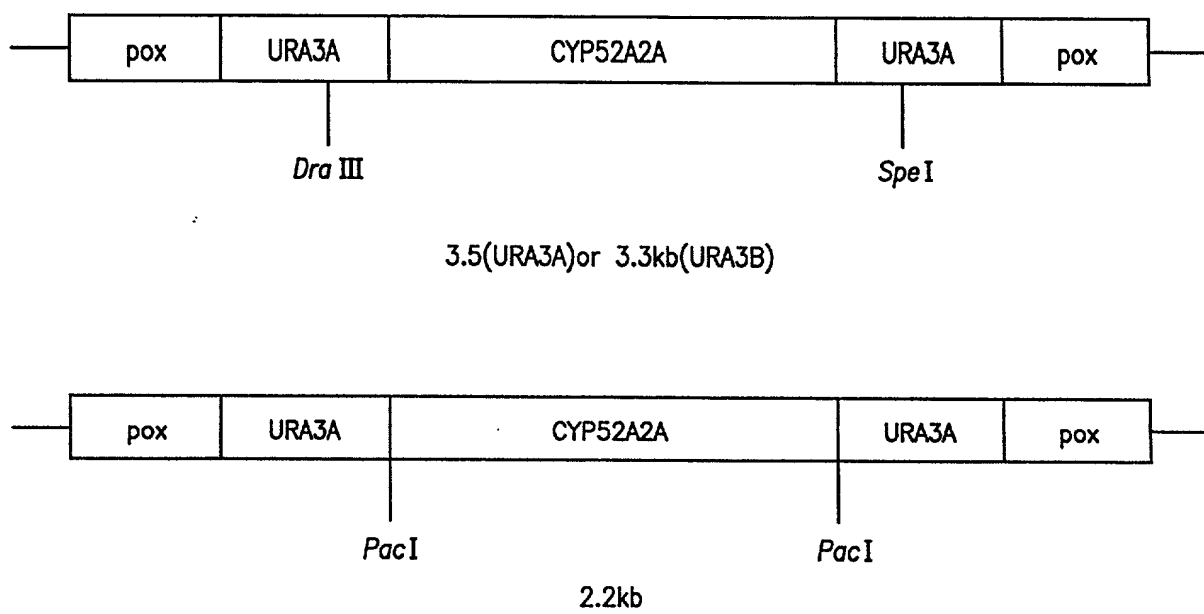


FIG. 28

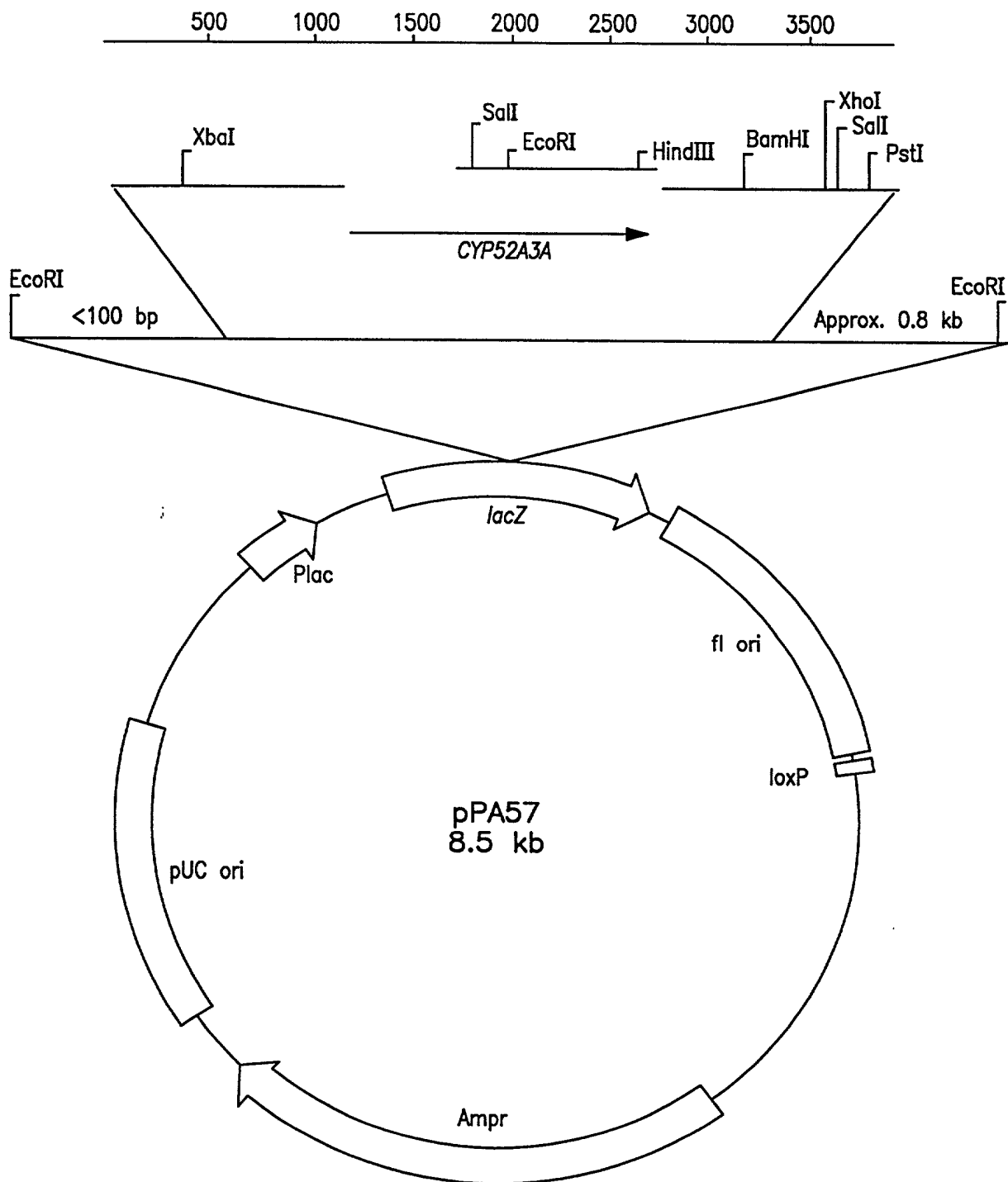


FIG. 29

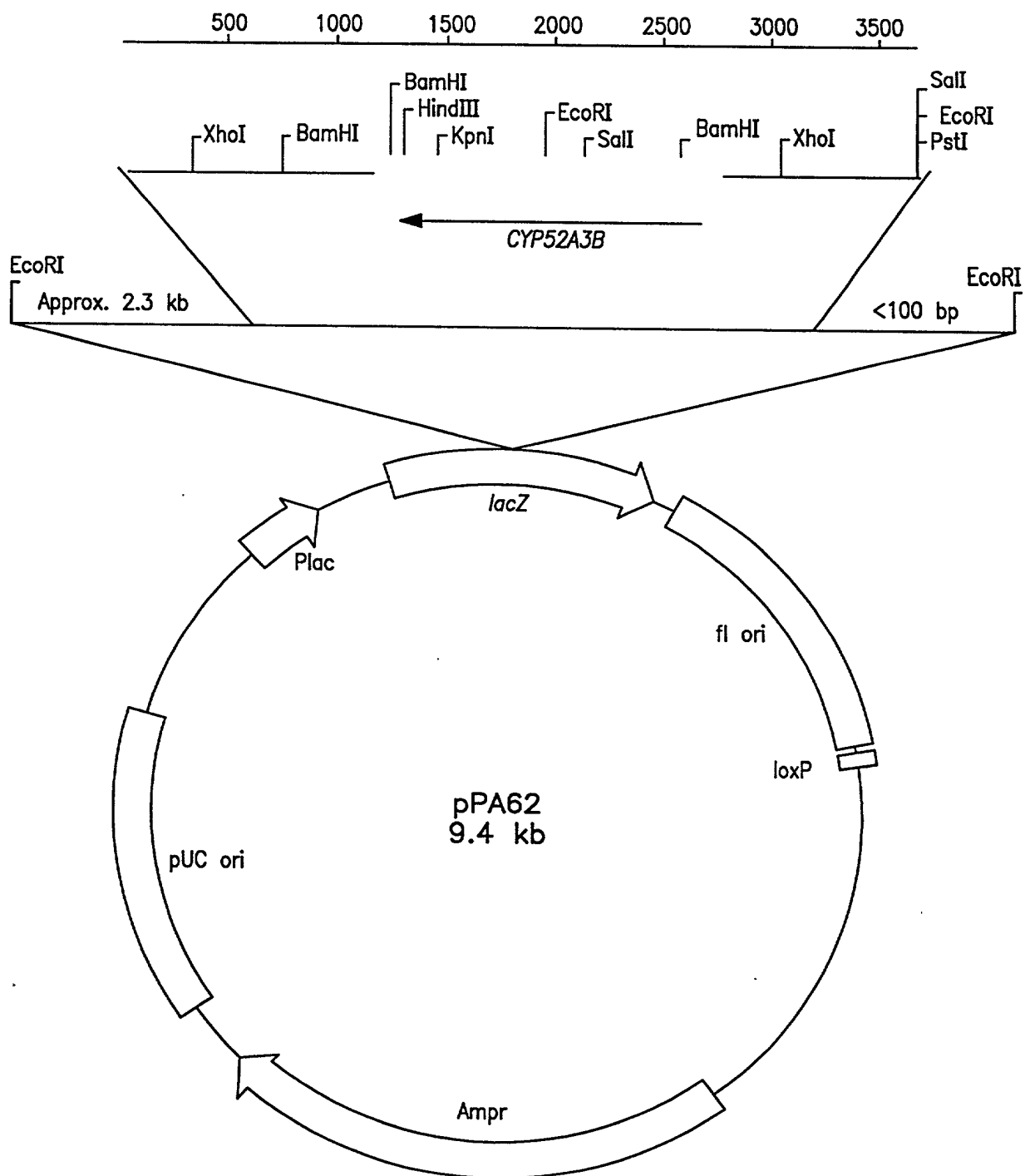


FIG. 30

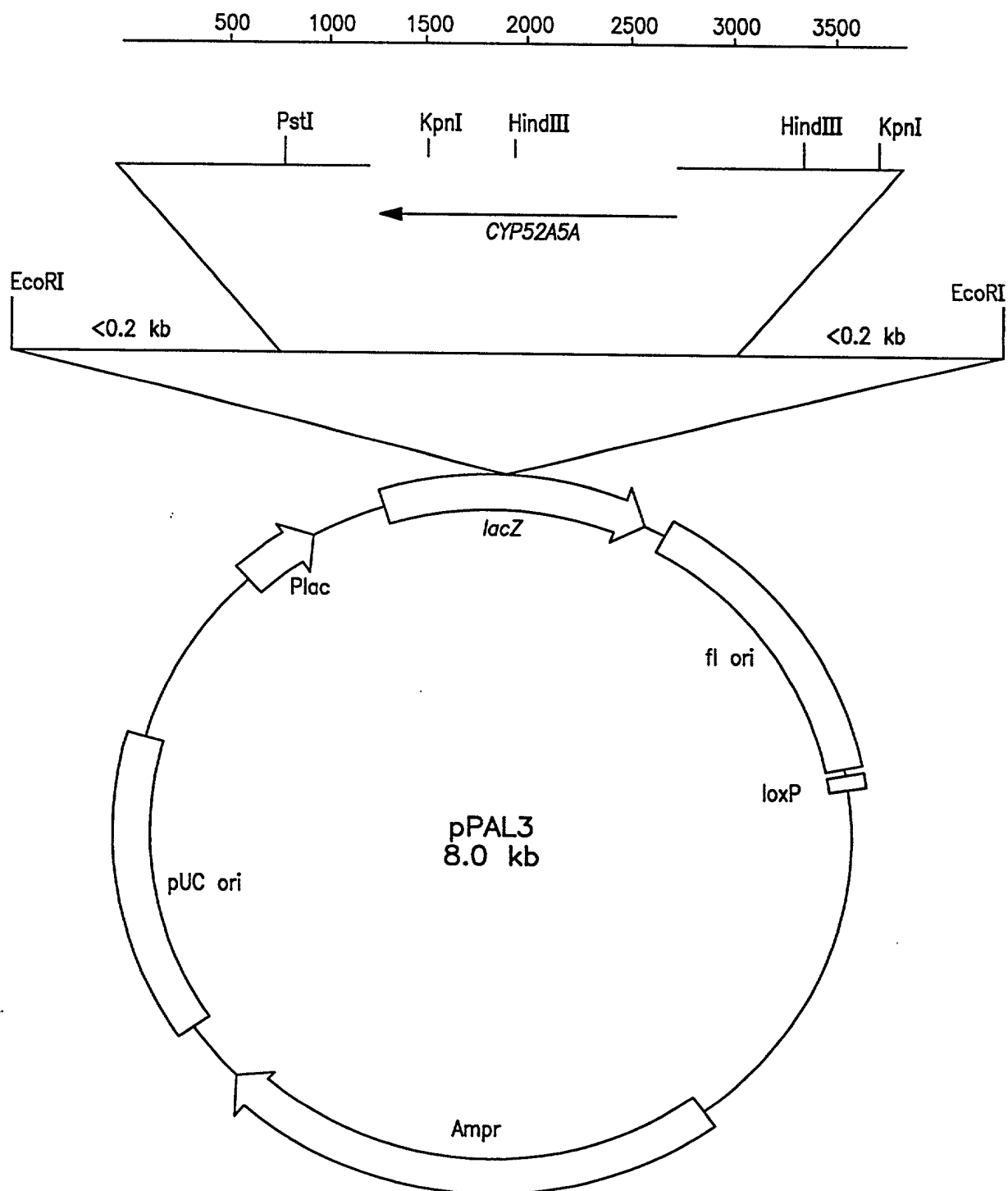


FIG. 3I

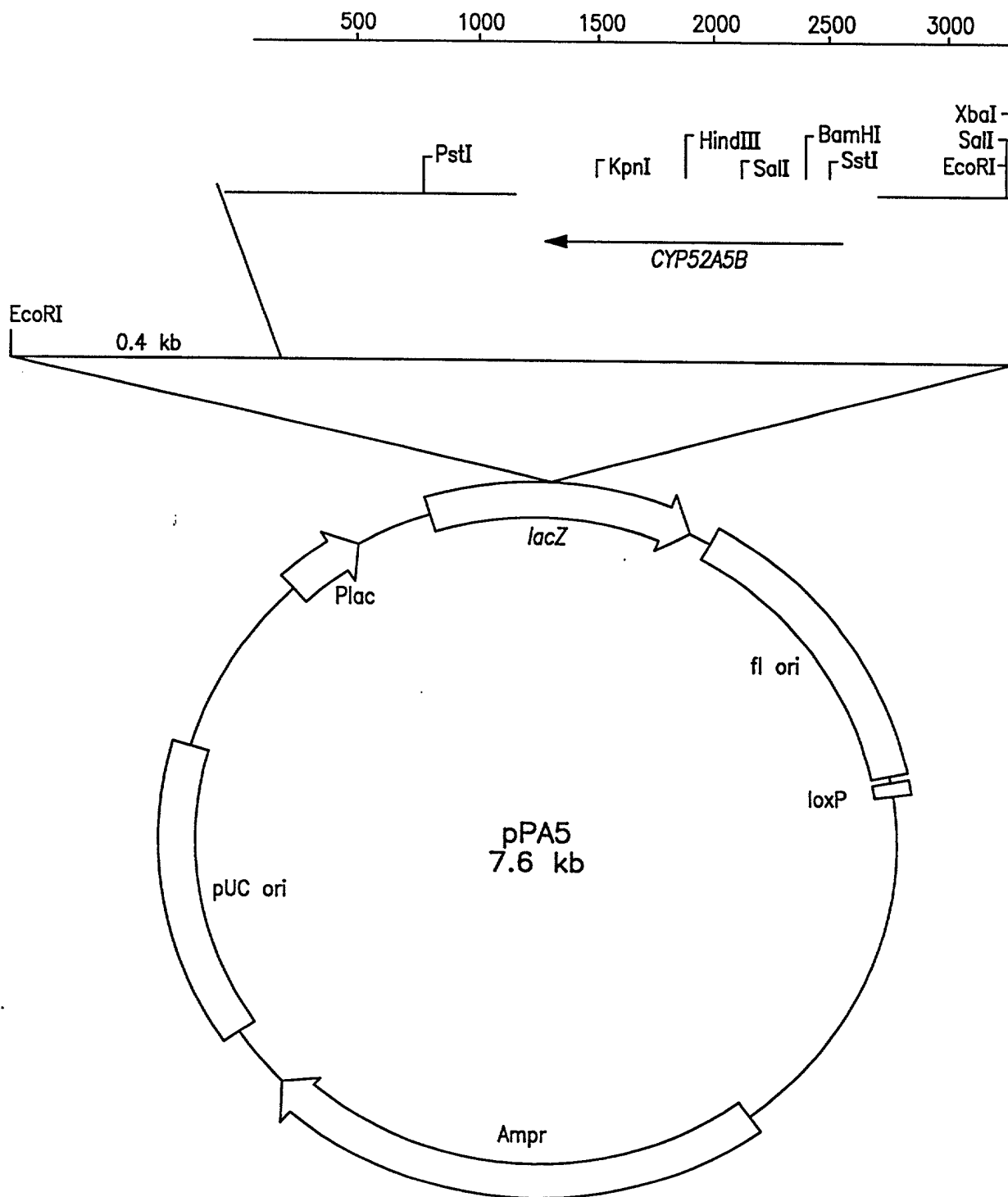


FIG. 32

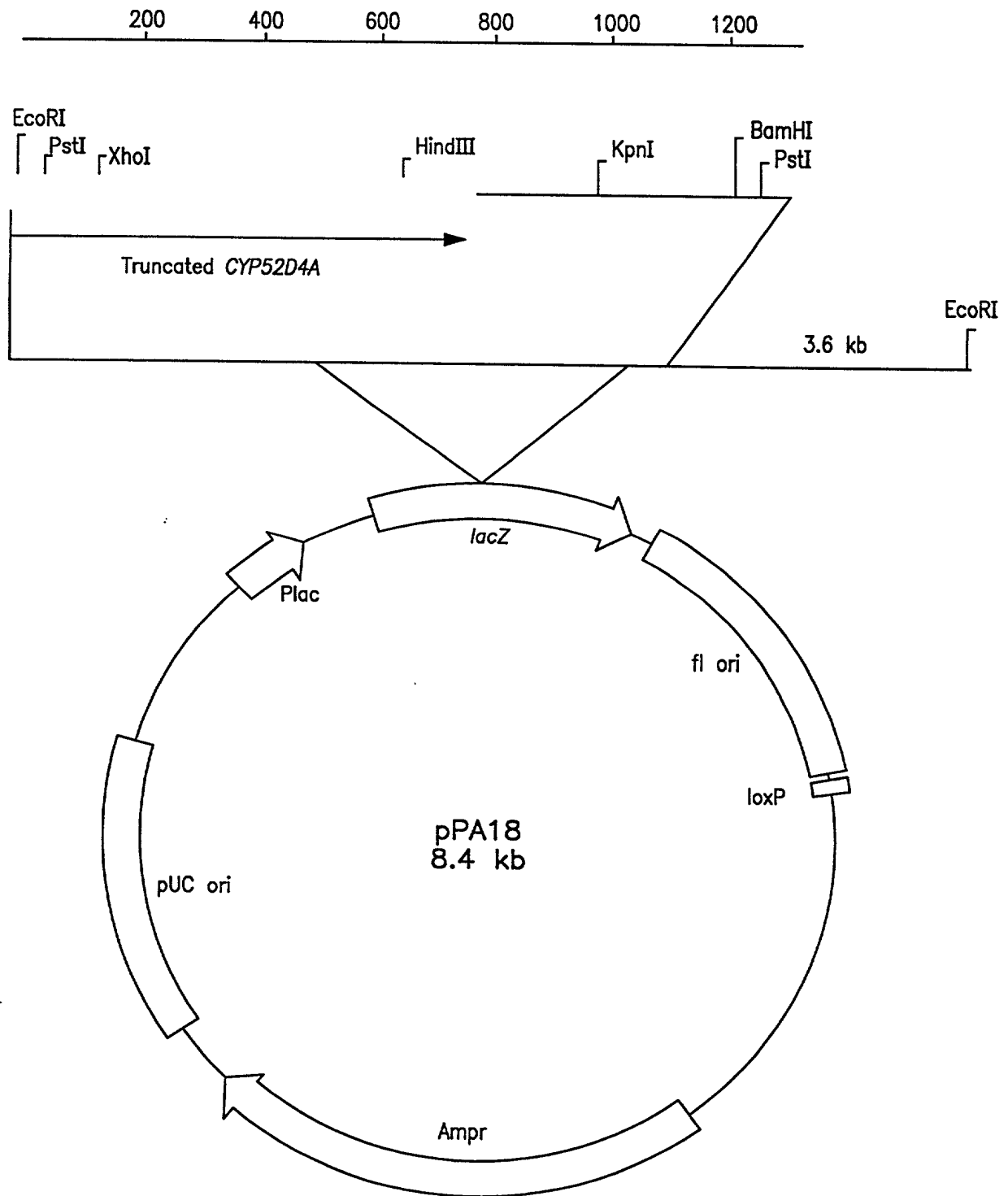


FIG. 33

Expression of CYP52A1, CYP52A2 and
CYP52A5 in Henkel Fermentor Run 3538-98

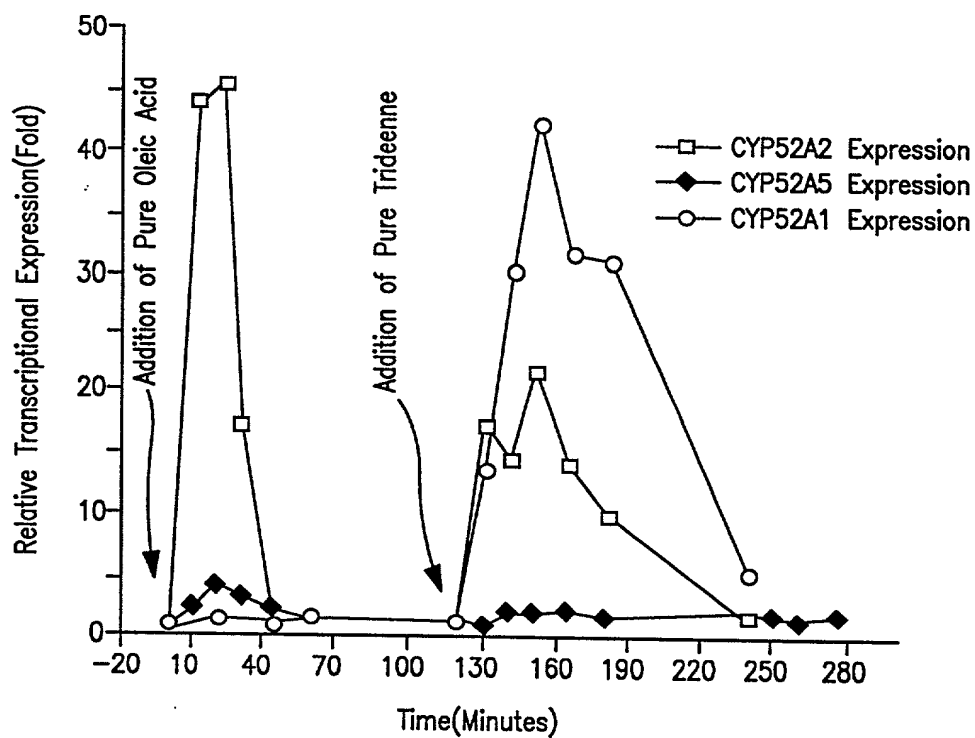
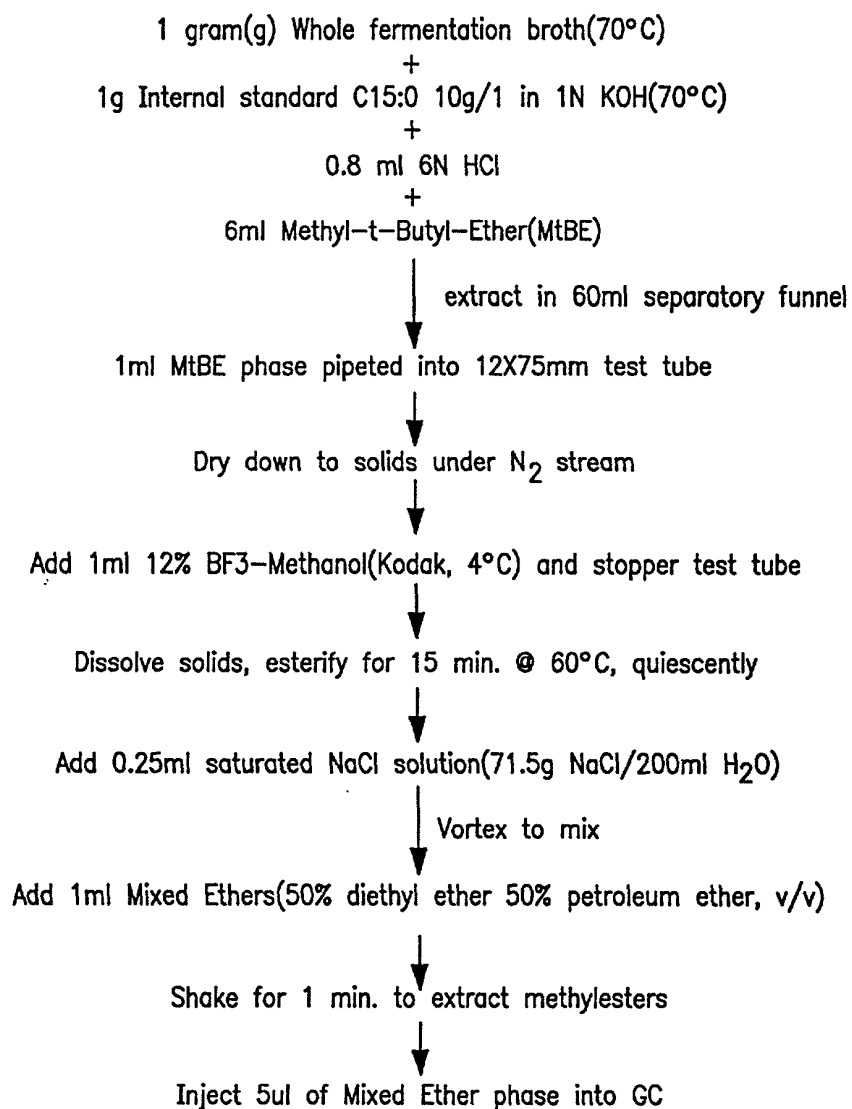


FIG. 34



GC parameters

Column : HP-INNOWAX capillary column, 30m X 0.32mm, 0.5 μm film thickness

Split Ratio : 1:100

Column Head Pressure : 13.5 psig

Injector Temperature : 240°C

FID Detector Temp. : 250°C

Temp. Prog. : 90°C for 0 min. to 190°C @ 7°C/min. for 0 min. to 235°C @ 12°C/min. for 30 min.

FIG. 35

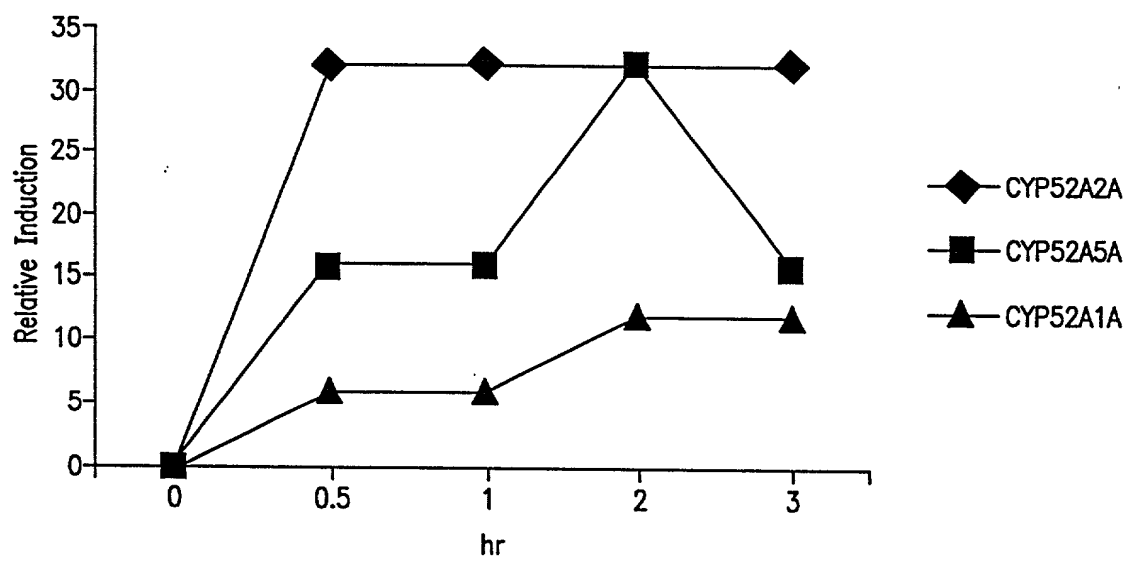


FIG. 36